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<p>(54) Title: COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE</p>		
<p>(57) Abstract</p> <p>Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.</p>		

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COMPOSITIONS ISOLATED FROM SKIN CELLS
AND METHODS FOR THEIR USE

5 Technical Field of the Invention

 This invention relates to polynucleotides encoding polypeptides, polypeptides expressed in skin cells, and various methods for treating a patient involving administration of a polypeptide or polynucleotide of the present invention.

10 Background of the Invention

 The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

15 Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in
20 cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed
25 from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

 The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty
30 tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous, glands and hair follicles.

Each strand of hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues.

5 The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence
10 growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents which protect skin against unwanted effects of sunlight.

15 Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins which play an important role in the inflammatory response against infection and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders
20 affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair are mediated by the effects of genes expressed in skin
25 and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune and inflammatory skin diseases more effectively and without adverse
30 effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding

proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.

Summary of the Invention

5 The present invention provides polypeptides expressed in skin cells, together with polynucleotides encoding such polypeptides, expression vectors and host cells comprising such polynucleotides, and methods for their use.

 In specific embodiments, isolated polynucleotides are provided that comprise a DNA sequence selected from the group consisting of: (a) sequences recited in SEQ
10 ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-
15 276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75% or 90% identity to a sequence of (a)-(d).

 In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a)
20 sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which comprise at least a functional portion of a
25 polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, are also provided.

30 In related embodiments, the present invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells, inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition
5 comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398.

10 Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 338 and 347; and (b) sequences having at least 50%, 75% or 90% identity to a sequence
15 provided in SEQ ID NOS: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 129 and 348; and (b) sequences having at
20 least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 129 and 348.

In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence
25 selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents
30 for the treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the

following more detailed description. All references disclosed herein are incorporated herein by reference in their entirety as if each was incorporated individually.

Brief Description of the Drawings

5 Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver; SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

 Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described
10 in the text.

 Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by muTR1a.

 Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

15 Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

 Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated murine splenocytes by KS2a.

 Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-
20 18) by a combination of KS3a plus apo-transferrin.

 Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1 (100 ng/ml), SDF1 α (100 ng/ml), and fMLP (10 μ M) on human PBMC.

 Figure 9 shows the chemotactic effect of muKS1 and SDF-1 α on THP-1 cells.

 Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after
25 intraperitoneal injections with muKS1 (50 μ g), GV14B (50 μ g) and PBS.

 Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in CV1/EBNA and HeLa cell lines by huTR1a.

 Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF α and PBS (100 ng/ml each).

30 Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells.

Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

Figure 15A shows the nucleotide sequence of KS1 cDNA (SEQ ID NO: 464) along with the deduced amino acid sequence (SEQ ID NO: 465) using single letter code. The 5' UTR is indicated by negative numbers. The underlined NH₂-terminal amino acids represent the predicted leader sequence and the stop codon is denoted by ***. The poly-adenylation signal is marked by a double underline. Figure 15B shows a comparison of the complete open reading frame of KS1 (referred to in Fig. 15B as KLF-1) with its human homologue BRAK and with the mouse α -chemokines mCrg-2, mMig, mSDF-1, mBLC, mMIP2, mKC and mLIX. An additional five residues are present in KS1 and BRAK between cysteine 3 and cysteine 4 that have not previously been described for chemokines.

Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated from mammalian skin cells. As used herein, the term "polynucleotide" means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and RNA molecules, both sense and anti-sense strands. The term comprehends cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki et al., *Artific. Organs* 20(8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be

used to amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All the polynucleotides provided by the present invention are isolated and purified, as those terms are commonly used in the art.

5 In specific embodiments, the polynucleotides of the present invention comprise a DNA sequence selected from the group consisting of sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, and variants of the sequences of SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464. Polynucleotides that comprise complements of such
10 DNA sequences, reverse complements of such DNA sequences, or reverse sequences of such DNA sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement," "reverse complement," and "reverse sequence," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse
15 sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

In another aspect, the present invention provides isolated polypeptides
20 encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide which comprises a partial isolated DNA sequence
25 provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as well as variants of such sequences.

Polypeptides of the present invention may be produced recombinantly by
30 inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may

be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin

Elmer/Applied BioSystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985).

- 5 Sections of DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

- 10 In certain preferred embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

- As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

- Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>) under `/blast/executables/`. The FASTA and FASTX

algorithms are available on the Internet at the ftp site <ftp://ftp.virginia.edu/pub/>. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX v1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, WR and Lipman, DJ, "Improved Tools for Biological Sequence Analysis," *PNAS* 85:2444-2448, 1988; and Pearson WR, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymology* 183:63-98, 1990.

The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described at NCBI's website at URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> and in the publication of Altschul, Stephen F., *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: `blastall -p blastn -d emblddb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results`; and parameters are: `-p` Program Name [String]; `-d` Database [String]; `-e` Expectation value (E) [Real]; `-G` Cost to open a gap (zero invokes default behavior) [Integer]; `-E` Cost to extend a gap (zero invokes default behavior) [Integer]; `-r` Reward for a nucleotide match (blastn only) [Integer]; `-v` Number of one-line descriptions (V) [Integer]; `-b` Number of alignments to show (B) [Integer]; `-i` Query File [File In]; `-o` BLAST report Output File [File Out] Optional. The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity for

polypeptides: blastall -p blastp -d swissprot -e 10 -G 1 -E 11 -r 1 -v 30 -b 30 -i queryseq -o results; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer];
 5 -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar
 10 portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

The percentage similarity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate
 15 algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage similarity. By way of example, a
 20 queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit
 25 in the EMBL database is thus 21/220 times 100, or 9.5%. The similarity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences
 30 by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is

interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an
5 E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides,
10 with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide
15 is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the
20 present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99%
25 probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited polynucleotide sequences under stringent conditions. As used herein, "stringent
30 conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in

1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465. The value of x may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, or of a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, or of a variant of one of the polypeptides provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465.

The inventive polynucleotides may be isolated by high throughput sequencing of cDNA libraries prepared from mammalian skin cells as described below in

Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain reaction (PCR) techniques. Probes can be shorter than the sequences provided herein but should be at least about 10, preferably at least about 15 and most preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by synthetic means using techniques well known in the art. Equipment for automated synthesis of oligonucleotides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived from skin, they likely encode proteins that have important roles in growth and development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25% similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as

modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states not only within skin, but also in
5 other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of
10 the inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the
15 above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

Alternatively, a vaccine or pharmaceutical composition of the present
20 invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines and pharmaceutical compositions, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems. Appropriate nucleic acid expression
25 systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*,
30 vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the art. The DNA

may also be "naked," as described, for example, in Ulmer, *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

5 Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from
10 about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per kg of host, and preferably from about 100 pg to about 1 μ g per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

 While any suitable carrier known to those of ordinary skill in the art may be
15 employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine,
20 talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

25 Any of a variety of adjuvants may be employed in the vaccines derived from this invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *M. tuberculosis*. Suitable
30 adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, New Jersey). Other suitable

adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Synteni (Palo Alto, California). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate corresponding ligand or receptor, as anti-inflammatory agents, and in compositions for skin, connective tissue and/or nerve tissue growth or regeneration.

Example 1

ISOLATION OF cDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

Table 1

<u>Library</u>	<u>Skin cell type</u>	<u>Source</u>
DEPA	dérmal papilla	rat
SKTC	keratinocytes	human
HNFF	neonatal foreskin fibroblast	human
MEMS	embryonic skin	mouse
KSCL	keratinocyte stem cell	mouse
<u>TRAM</u>	<u>transit amplifying cells</u>	<u>mouse</u>

These cDNA libraries were prepared as described below.

cDNA Library from Dermal Papilla (DEPA)

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA Library from Keratinocytes (SKTC)

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoloff, B in *Handbook of Keratinocyte Methods*, pp. 17-24, 1994) were grown in serum-free KSFM (BRL Life Technologies) and harvested along with differentiated cells (10^8 cells). Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final concentration of 10% to the culture medium and cells were harvested after 48 hours. Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two populations of cDNA were separately digested with *RsaI* to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and Berkowitz, GA, *BioTechniques* 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid DNA for sequencing.

cDNA library from human neonatal fibroblasts (HNFF)

Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life

Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA library from mouse embryonic skin (MEMS)

Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice. Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharmingen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse CD45 phycoerythrin conjugated monoclonal antibody (Pharmingen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin $\beta 1$ chain. CD45, a leucocyte specific

antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as KSCL), and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer.

Example 2

CHARACTERIZATION OF ISOLATED CDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding predicted protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithms FASTX and/or BLASTP. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX) were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt database (using BLASTP) were made as of January 23, 1999. Comparisons of polynucleotide sequences provided in SEQ ID NO: 418-455 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ

ID NO: 456-463 to sequences in the SwissProt database (using BLASTP) were made as of April 23, 2000.

Isolated cDNA sequences and their corresponding predicted protein sequences were computer analyzed for the presence of signal sequences identifying secreted molecules. Isolated cDNA sequences that have a signal sequence at a putative start site within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, 399, 418-434 and 440-449. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, 356-358 and 440 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms FASTA or BLASTN, as described above. The predicted amino acid sequences of SEQ ID NO: 120-125, 275-276, 373-380 and 382 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of the full-length cDNA sequences provided in SEQ ID NOS: 7-14, 200-231, 372, 418-422, 441-448. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 7-14, 200-231 and 372 are provided in SEQ ID NOS: 126-133, 277-308 and 396, respectively. The cDNA sequences of SEQ ID NO: 418-422 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO 7 and 11-14, namely SEQ ID NO: 126, and 130-133, respectively.

Comparison of the full length cDNA sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences. Comparison of the amino acid sequences provided in SEQ ID NOS: 126-133 and 277-308 with those in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NOS: 15-23 with those in the EMBL database using the computer algorithm FASTA database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NOS: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NOS: 24-44, 232-238, 423-434 and 449. The amino acid sequences encoded by the cDNA sequences of

SEQ ID NO: 24-44, 232-238 and 429 are provided in SEQ ID NOS: 143-163, 309-315 and 456, respectively. The cDNA sequences of SEQ ID NO: 423-428, 430-434 and 449 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 27-29, 34, 35, 37, 40-44 and 238, namely SEQ ID NO: 146-148, 153, 154, 156, 159-163 and 315, respectively. These amino acid sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose corresponding predicted protein sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have either one or more transmembrane domain(s) within the sequence are provided in SEQ ID NOS: 45-63, 239-253, 359-364, 400-402, 435, 436, 450-452 and 455. The cDNA sequences of SEQ ID NOS: 45-48, 239-249, 359-361, 363, 450, 451 and 455 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 45-48, 239-249, 359-361, 363, 450 and 451 (provided in SEQ ID NOS: 164-167, 316-326, 383, 385-388, 407-408, 460 and 461, respectively) were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX or BLASTP database. The cDNA sequence of SEQ ID NO: 455 encodes the same amino acid sequence as the cDNA sequence of SEQ ID NO: 359, namely SEQ ID NO: 383.

Comparison of the amino acid sequences corresponding to the cDNA sequences of SEQ ID NOS: 49-63, 250-253, 436 and 452 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NOS: 168-182, 327-330, 457 and 462, respectively.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode predicted protein sequences that appear to be family members of known protein families. A family member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NOS: 64-76, 254-264, 365-369, 403, 437-439, 453 and 454. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 64-76, 254-264, 365-369, 403, 438, 439 and 453 are provided in SEQ ID NOS: 183-195, 331-341, 389-393, 409, 458, 459 and 463, respectively.

The cDNA sequences of SEQ ID NO: 437 and 454 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 68 and 262, namely SEQ ID NO: 187 and 339, respectively. The cDNA sequences of SEQ ID NOS: 64-68, 254-264, 365-369, 453 and 454 show less than 75% identity (determined as described above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of SEQ ID NOS: 183-195, 331-341, 389-393, 458, 459 and 463 show less than 75% identity to sequences in the SwissProt database.

The utility for each of the proteins encoded by the DNA sequences of SEQ ID NOS: 64-76, 254-264, 365-369, 403, 438, 439, 453 and 454, based on similarity to known proteins, is provided below:

Table 2
FUNCTIONS OF NOVEL PROTEINS

P/N SEQ ID NO.	A/A SEQ ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
64, 372	183, 396	Slit, a secreted molecule required for central nervous system development
65	184	Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains
66, 403	185, 409	RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis
67	186	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation
68, 437	187	Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes
69	188	DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes
70	189	A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors
71	190	Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes
72	191	Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes.
73, 438	192, 458	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
74	193	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors
75, 439	194, 459	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
76	195	Immunoglobulin receptor family
254	331	Receptor with immunoglobulin-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors
255	332	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells.

P/N SEQ ID NO:	A/A SEQ. ID NO:	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		EGF is involved in wound healing. It also inhibits gastric acid secretion.
256	333	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
257	334	Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation.
258	335	Notch family proteins which are receptors involved in cellular differentiation.
259	336	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation.
260, 453	337, 463	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors.
261	338	Immunoglobulin receptor family
262, 454	339	ADP/ATP transporter family member containing a calcium binding site.
263	340	Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes
264	341	Nucleotide-sugar transporter family member.
365	389	Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation.
366	390	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
367	391	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
368	392	Cell wall protein precursor. Are involved in cellular growth or differentiation.
369	393	HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.

These isolated sequences thus encode proteins that influence the growth, differentiation and activation of several cell types. They may usefully be developed as agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease.

5 The polynucleotide sequences of SEQ ID NOS: 77-117, 265-267 and 404-405 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 10 1997). The sequences of SEQ ID NOS: 77-89, 265-267 and 365-369 were determined to have less than 75% identity to sequences in the EMBL and SwissProt databases using the computer algorithm FASTA or BLASTN, as described above. The proteins encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins 15 may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

20

Example 3

ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF muTR1

25 The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, 30 with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 196. The library was screened using an [α ³²P]-dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO:

118.

The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF). This EGF-like protein will serve to stimulate keratinocyte growth and motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of epithelial-derived cancers.

Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with [α^{32} P]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huTR1 was 3.5-4kb in size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus prostate and ovary (Fig. 1).

The high abundance of mRNA for huTR1 in the heart and placenta indicates a role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of Transforming Growth Factor-alpha and EGF to induce *de novo* development of blood vessels (Schreiber, *et al.*, *Science* 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, *et al.*, *Science* 232:1250-1253, 1986), and their over-expression in a variety of human tumors.

Purification of muTR1 and huTR1

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These

constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *ibid*.

5 Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100 µg/ml ampicillin. This culture was spun down and used to inoculate 500 ml culture of Terrific broth containing 100 µg/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) and that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in 10 insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication 15 on ice at 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The 20 pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove debris. The supernatant was stored at 4 °C until use.

25 Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the protein solution was added to 5x its volume of refolding buffer (1 mM 30 EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly

during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

Biological Activities of Polypeptides muTR1a and huTR1a

5 muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGF α , epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of
10 MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

 In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line
15 A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were stimulated in the same way with 10 to 100 ng/ml TGF-alpha or EGF. As a negative control, cells were stimulated with PBS containing varying
20 amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15 μ g of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins were then transferred to PVDF membrane using standard techniques.

 For Western blotting, membranes were incubated in blocking buffer (10mM
25 Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were washed for 30 mins in blocking buffer minus non-fat milk before being incubated with anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking
30 buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus

non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for 5 to 30 min.

As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1 and huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were conducted as described above. This indicates that huTR1a acts as a ligand for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine pituitary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human transforming growth factor alpha (huTGF α) or PBS-BSA was titrated into the plates and 1×10^3 NF keratinocytes were added to each well. The plates were incubated for 5 days in an atmosphere of 5% CO₂ at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 3, both muTR1a and the positive control human TGF α stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies) supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and 1×10^3 HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% CO₂ at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982), and cell death was determined using the MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in angiogenesis and vascularization of tumors. This novel gene and its encoded protein may thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.

Upregulation of huTR1 and mRNA expression

HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of 1×10^6 cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGF α , or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland). Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1 μ l of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5 μ l of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGF α can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGF α can up-regulate

the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGF α .

Serum response element reporter gene assay

5 The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed keratinocytes), containing eight SRE upstream of an
10 SV40 promotor and luciferase reporter gene were developed in-house. 5×10^3 cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma, St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine
15 (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then
20 stimulated with a titration of TR1 from 1 μ g/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40 μ l of lysis buffer (Promega). 10 μ l was
25 transferred to a 96 well plate and 10 μ l of luciferase substrate (Promega) added by direct injection into each well by a Victor² fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

30 As shown in Fig. 13, muTR1 activated the SRE in both PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a

growth response. In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response. Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets. TR1 may also be important in the development and progression of neural tumors.

5

Inhibition by the EGF receptor assay

The HaCaT growth assay was conducted as previously described, with the following modifications. Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or the
10 negative control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibited the mitogenicity of TR1 on HaCaT cells. This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells. TR1 may bind
15 directly to the EGF receptor. TR1 may also bind to any other members of the EGFR family (for example, ErbB-2, -3, and/or -4) that are capable of heterodimerizing with the EGFR.

Splice variants of huTR1

A variant of huTR1 was isolated from the same library as huTR1, following the same protocols. The sequence referred to as huTR1-1 (also known as TR1 δ) is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 15 to 44 and 87 to 137. These deletions have the effect of deleting part of the signal sequence and following amino terminal linker sequence, residues following the second cysteine residue of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1-1 is an intracellular form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined nucleotide sequence of huTR1-1, is given in SEQ ID NO: 412, with the corresponding amino acid sequence being provided in SEQ ID NO: 415.

Four additional splice variants of huTr1 were isolated by PCR on first strand cDNA made from RNA isolated from HeLa cells by standard protocols. These splice variants of huTR1 are referred to as TR1-2 (also known as TR1 β), TR1-3 (also known as TR1 γ), TR1 ϵ and TR1 ϕ .

TR1-2 consists of the ORF of huTR1 minus amino acids 95 to 137. This deletion has the effect of deleting the transmembrane domain. Therefore TR1-2 is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined cDNA sequence of TR1-2 is given in SEQ ID NO: 410 and the corresponding amino acid sequence in SEQ ID NO: 413.

TR1-3 consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 86 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence, residues following the second cysteine of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1-3 is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and

TGF α . The determined cDNA sequence of TR1-3 is given in SEQ ID NO: 411 and the corresponding amino acid sequence is SEQ ID NO: 414.

TR1 ϵ consists of the ORF of huTR1 minus amino acids 86 to 136. This deletion has the effect of deleting residues following the second cysteine of the EGF motif and the transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1 ϵ is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined cDNA sequence of TR1 ϵ is given in SEQ ID NO: 371 and the corresponding predicted amino acid sequence in SEQ ID NO: 395.

TR1 ϕ consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 95 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence and the transmembrane domain. Therefore TR1 ϕ is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined nucleotide sequence of TR1 ϕ is given in SEQ ID NO: 416 and the corresponding predicted amino acid sequence in SEQ ID NO: 417.

Example 4

IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by standard cell biology techniques. This double stranded cDNA was labeled with [α^{32} P]- dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization and screening were performed using standard molecular biology techniques.

Example 5

ISOLATION AND CHARACTERIZATION OF KS1

Analysis of RNA transcripts by Northern Blotting

5 Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [α^{32} P]-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was
10 observed to be most abundant in brain, lung, or any muscle, and heart. Expression could also be detected in lower intestine, skin, bone marrow, and kidney. No detectable signal was found in testis, spleen, liver, thymus, stomach.

Human homologue of muKS1

MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release
15 50, plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified in AA643952 and HS1301003 when translated. Combination of all three
20 ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

Identification of KSCL009274 cDNA sequence

25 A directionally cloned cDNA library was constructed from immature murine keratinocytes and submitted for high-throughput sequencing. Sequence data from a clone designated KDCL009274 showed 35% identity over 72 amino acids with rat macrophage inflammatory protein-2B (MIP-2B) and 32% identity over 72 amino acids with its murine homologue. The insert of 1633bp (SEQ ID NO: 464; Fig. 15A)
30 contained an open reading frame of 300bp with a 5' untranslated region of 202bp and a 3' untranslated region of 1161bp. A poly-adenylation signal of AATAAA is present 19 base pairs upstream of the poly-A tail. The predicted mature polypeptide (SEQ ID

NO: 465) is 77 amino acids in length containing 4 conserved cysteines with no ELR motif. The putative signal peptide cleavage site between GLY 22 and Ser 23 was predicted by the hydrophobicity profile. This putative chemokine was identical to KS1. The full length sequence was screened against the EMBL database using the BLAST program and showed some identity at the nucleotide level with human EST clones AA643952, AA865643, and HS1301003, respectively. A recently described human CXC chemokine, BRAK, has some identity with KS1 at the protein level. The alignment of KS1 (referred to in Fig. 15B as KLF-1), BRAK, and other murine α -chemokines is shown in Fig. 15B. The phylogenetic relationship between KS1 and other α -chemokine family members was determined using the Phylip program. KS1 and BRAK demonstrate a high degree of divergence from the other α -chemokines, supporting the relatively low homology shown in the multiple alignment.

Bacterial expression and purification of muKS1 and huKS1

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids 23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen, Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid*.

Starter cultures of recombinant BL 21 (DE3) *E. coli* (Novagen) containing SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY broth containing 100 μ g/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 μ g/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM β -Mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were

further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5 + 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% (w/v) glycerol. Preparations obtained were greater than 95% pure as determined by SDS-PAGE. Endotoxin contamination of purified proteins were determined using a limulus amebocyte lysate assay kit (BIO Whittaker, Walkersville, MD). Endotoxin levels were <0.1 ng/μg of protein. Internal amino acid sequencing was performed on tryptic peptides of KS1.

An Fc fusion protein was produced by expression in HEK 293 T cells. 35μg of KLF-1pIGFc DNA to transfect 6×10^6 cells per flask, 200 mls of Fc containing supernatant was produced. The Fc fusion protein was isolated by chromatography using an Affiprep protein A resin (0.3 ml column, Biorad). After loading, the column was washed with 15 mls of PBS, followed by a 5 ml wash of 50 mM Na citrate pH 5.0. The protein was then eluted with 6 column volumes of 50 mM Na citrate pH 2.5, collecting 0.3 ml fractions in tubes containing 60μl of 2M Tris-HCl pH 8.0. Fractions were analyzed by SDS-PAGE.

Peptide sequencing of muKS1 and huKS1

Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa. To obtain the amino acid sequence of the 15 kDa bands, 20 µg recombinant muKS1 and huKS1 was resolved by SDS-PAGE and electroblotted onto Immobilon PVDF membrane (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that the determined sequences are identical to those predicted from the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A, Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordoni R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR, Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization," *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California). Recombinant Fc tagged KS1 expressed and purified using protein A affinity column chromatography revealed a homogenous protein with a molecular mass of 42kDa.

Oxidative burst assay

Oxidative burst assays were used to determine responding cell types. 1×10^7 PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and incubated for 30 minutes at 37°C with 5 μ l 5 mM dichloro-dihydrofluorescein diacetate (H₂DCFDA, Molecular Probes, Eugene, Oregon). 2 x 10⁵ H₂DCFDA-labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 μ l of each agonist was added simultaneously into the well of the flat-bottomed plate to give final concentrations of 100 ng/ml (fMLP was used at 10 μ M). The plate was then read on a Victor² 1420 multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation wavelength and 535 nm emission wavelength. Relative fluorescence was measured at 5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold difference between control treated cells (TR1) and cells treated with 100 ng/ml muKS1 (Fig. 8). Human stromal derived factor-1 α (SDF1 α) (100 ng/ml) and 10 μ M formyl-Met-Leu-Phe (fMLP) were used as positive controls.

Chemotaxis assay

Cell migration in response to muKS1 was tested using a 48 well Boyden's chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and added to the bottom wells of the chemotactic chamber. THP-1 cells were resuspended in the same buffer at 3×10^5 cells per 50 μ l. Top and bottom wells were separated by a PVP-free polycarbonate filter with a 5 μ m pore size for monocytes or 3 μ m pore size for lymphocytes. Cells were added to the top well and the chamber incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO₂ humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped from the upper surface. The filter was then stained with Diff-Quick (Dade International Inc., Miami, Florida) and the number of migrating cells counted in five randomly selected high power fields. The results are expressed as a migration index (the number of test migrated cells divided by the number of control migrated cells).

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml (Fig. 9). Human SDF1 α was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no migration was evidence for muKS1 even at high concentrations, whereas SDF-1 α provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

Flow cytometric binding studies

Binding of KLF-1 to THP-1 and Jurkat cells was tested in the following manner. THP-1 or Jurkat cells (5×10^6) were resuspended in 3 mls of wash buffer (2% FBS and 0.2% sodium azide in PBS) and pelleted at 4°C, 200g for 5 minutes. Cells were then blocked with 0.5% mouse and goat sera for 30 minutes on ice. Cells were washed, pelleted, resuspended in 50 μ l of KLF-1Fc at 10 μ g/ml and incubated for 30 minutes on ice. After incubation, the cells were prepared as before and resuspended in 50 μ l of goat anti-human IgG biotin (Southern Biotechnology Associates, AL) at 10 μ g/ml and incubated for 30 minutes on ice. Finally, cells were washed, pelleted and resuspended in 50 μ l of streptavidin-RPE (Southern Biotechnology Associates, AL) at 10 μ g/ml and incubated for a further 30 minutes on ice in the dark. Cells were washed and resuspended in 250 μ l of wash buffer and stained with 1 μ l of 10 μ g/ml propidium iodide (Sigma) to exclude any dead cells. Purified Fc fragment (10 μ g/ml) was used as a negative control in place of KLF-1Fc to determine non-specific binding. Ten thousand gated events were analyzed on log scale using PE filter arrangement with peak transmittance at 575nm and bandwidth of 10nm on an Elite cell sorter (Coulter Cytometry).

The respiratory burst and migration assays indicated that KS1 is active on monocytes and not T cells; therefore, the KS1 Fc fusion protein was tested in a binding study with THP-1 and Jurkat T cells. KS1 Fc showed a marked positive shift on THP-1 cells compared with the Fc fragment alone. In contrast, KS1 demonstrated no positive binding with Jurkat cells in an identical experiment.

Full length sequence of muKS1 clone

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in
5 SEQ ID NO: 394.

Analysis of human RNA transcripts by Northern blotting

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots
10 (Clontech, Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in
15 pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.

Analysis of human RNA transcripts in tumor tissue by Northern blotting

Northern blot analysis to determine distribution of huKS1 in cancer tissue was
20 performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either
25 ovary or ovarian tumors.

Injection of bacterially recombinant muKS1 into C3H/HeJ mice

Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B
30 is a bacterially expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18

hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual mice from each group. Mice injected with 50 µg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

5 20 µg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an
10 inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

Injection of bacterially expressed muKS1a into nude mice

To determine whether T cells are required for the inflammatory response, the
15 experiment was repeated using nude mice. Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered
20 saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline.
25 Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

30 Discussion

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini, *et al.*, *Annu. Rev. Immunol.*, 15:675-705,

1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore
5 be expected to stimulate leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to
10 chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid,
15 stromal, and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 promotes a quantifiable increase in cell
20 numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 induces an oxidative burst in human peripheral blood mononuclear cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at
25 high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-
30 regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA tumor," *J. Immunol.*

161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998). Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal carcinoma.

Example 6

CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

Mammalian Expression

To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid.* The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using

DEAE-dextran. The supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes was determined as follows.

5 A single cell suspension was prepared from the spleens of BALB/c mice and washed into DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arginine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate, 5×10^{-2} mM beta mercaptoethanol and 5% FCS (cDMEM). Splenocytes (4×10^6 /ml) were stimulated with 2 ug/ml concanavalin A

10 for 24 hrs at 37°C in 10% CO₂. The cells were harvested from the culture, washed 3 times in cDMEM and resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at 1×10^5 cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and 1×10^4 activated T cells (0.1 ml) were added to each well. The

15 plates were incubated for 2 days in an atmosphere containing 10% CO₂ at 37°C. The degree of proliferation was determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a

20 was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS, BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This suggests a role for KS2 in the regulation of skin inflammation and malignancy.

25

Example 7

Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature

30 polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial

cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with 750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and 1×10^3 IEC-18 cells were added to each well. The plates were incubated for 5 days at 37°C in an atmosphere containing 10% CO_2 . The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of epithelial cells of the intestine. This suggests a role for KS3 in wound healing, protection from radiation- or drug-induced intestinal disease, and integrity of the epithelium of the intestine.

SEQ ID NOS: 1-465 are set out in the attached Sequence Listing. The codes for polynucleotide and polypeptide sequences used in the attached Sequence Listing confirm to WIPO Standard ST.25 (1988), Appendix 2.

All references cited herein, including patent references and non-patent references, are hereby incorporated by reference in their entireties.

Although the present invention has been described in terms of specific embodiments, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (e) sequences having at least a 99% probability of being the same as a sequence selected from any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters described above; and (f) nucleotide sequences having at least 50% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
2. An expression vector comprising an isolated polynucleotide of claim 1.
3. A host cell transformed with an expression vector of claim 2.
4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters described above; and (c) sequences having at least 50% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
5. An isolated polynucleotide encoding a polypeptide of claim 4.

6. An expression vector comprising an isolated polynucleotide of claim 5.
7. A host cell transformed with an expression vector of claim 6.
- 5 8. An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-10 415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters described above; and (c) sequences having at least 50% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.
- 15 9. A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.
- 20 10. The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; (b) sequences having at least about 50% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.
- 25 11. A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.
- 30 12. The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (b) sequences having at least 50% identity to a sequence of

SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

13. A method for modulating angiogenesis in a patient, comprising
5 administering to the patient a composition comprising a polypeptide of claim 4.

14. The method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence of
10 SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

15. A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising a
15 polypeptide of claim 4.

16. The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence
20 of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

17. A method for modulating skin inflammation in a patient, comprising
25 administering to the patient a composition comprising a polypeptide of claim 4.

18. The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 338 and 347; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running
30 parameters and identity test defined above.

19. A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

5 20. The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 129 and 348; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

10 21. A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

15 22. The method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

20 23. A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

25 24. The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

30 25. A method for treating cancer in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

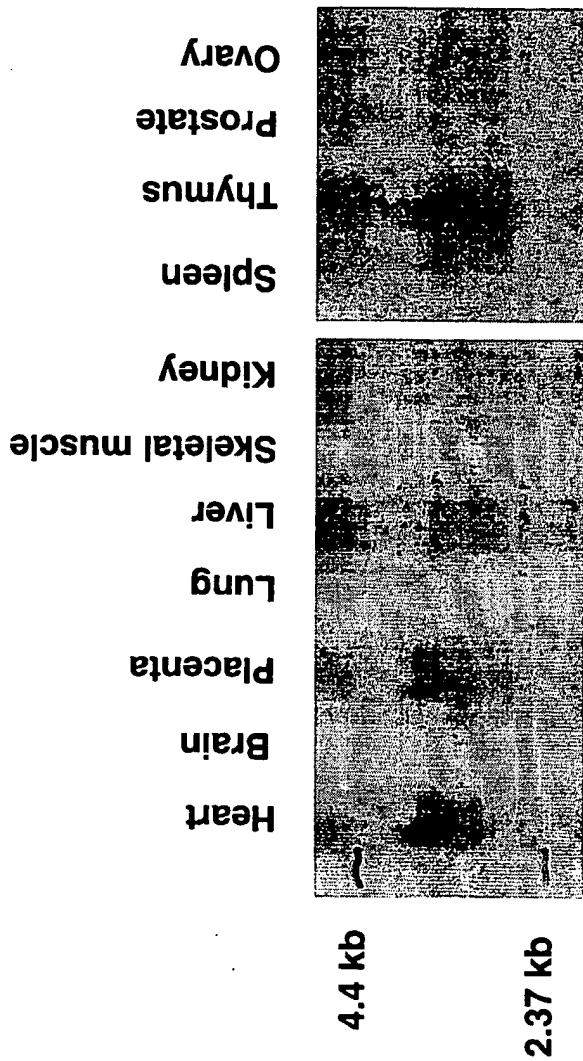
26. The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

27. A method for treating a neurological disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

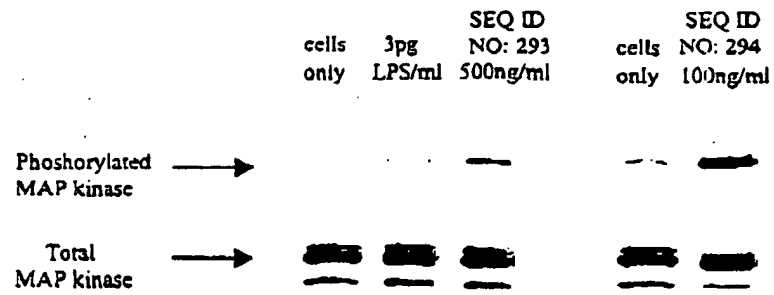
28. The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

Figure 1

Distribution of human TAK1 mRNA in human tissues

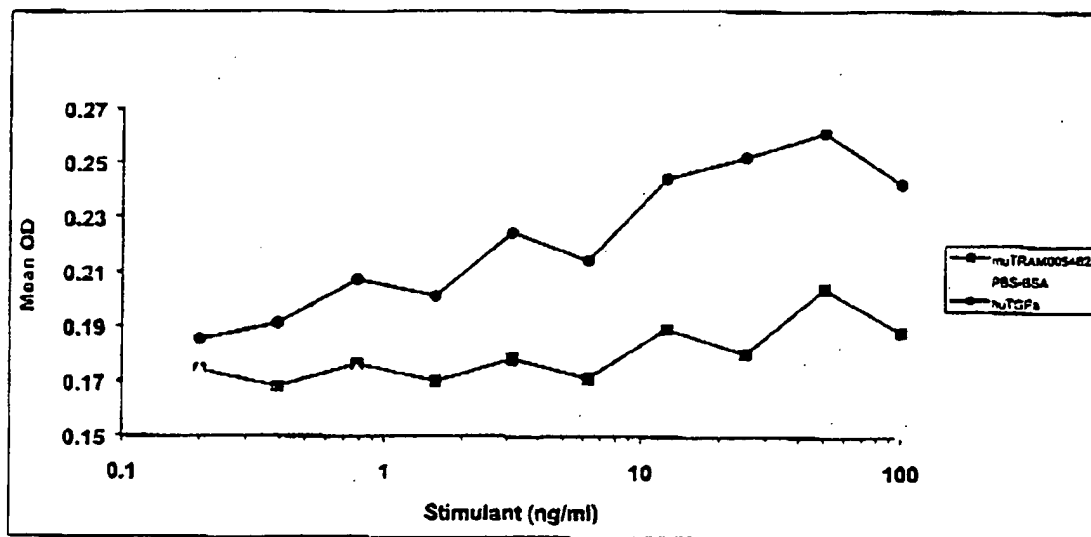


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Figure 2

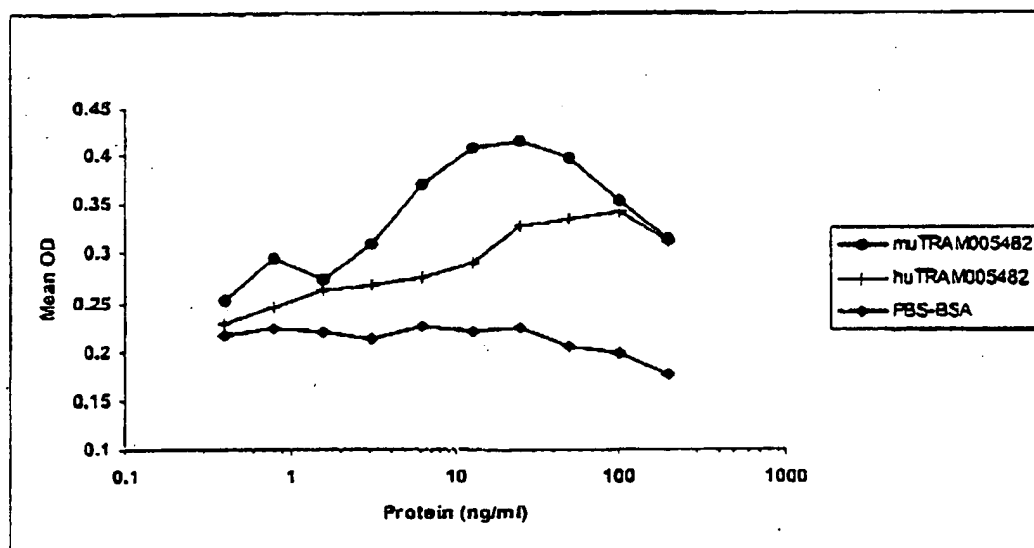
3/16

Figure 3



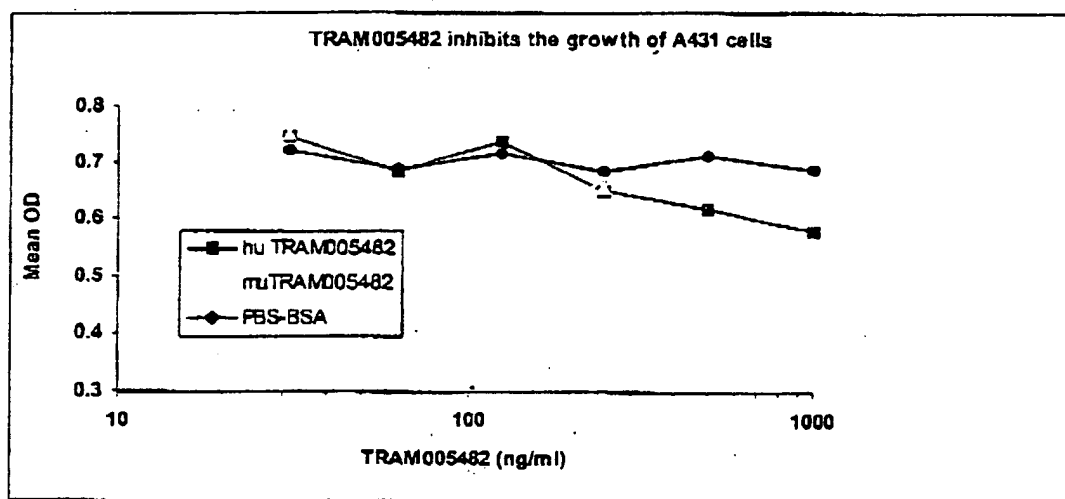
4/16

Figure 4



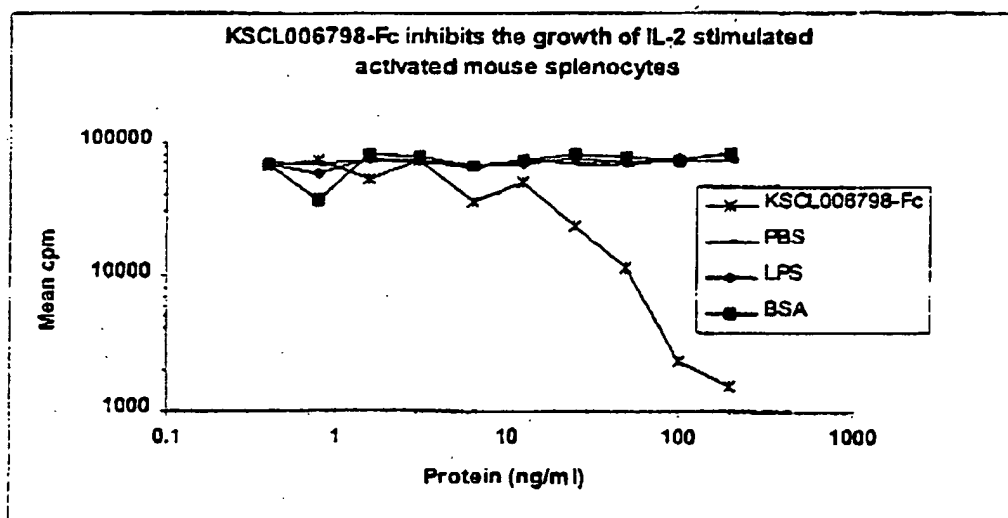
5/16

Figure 5



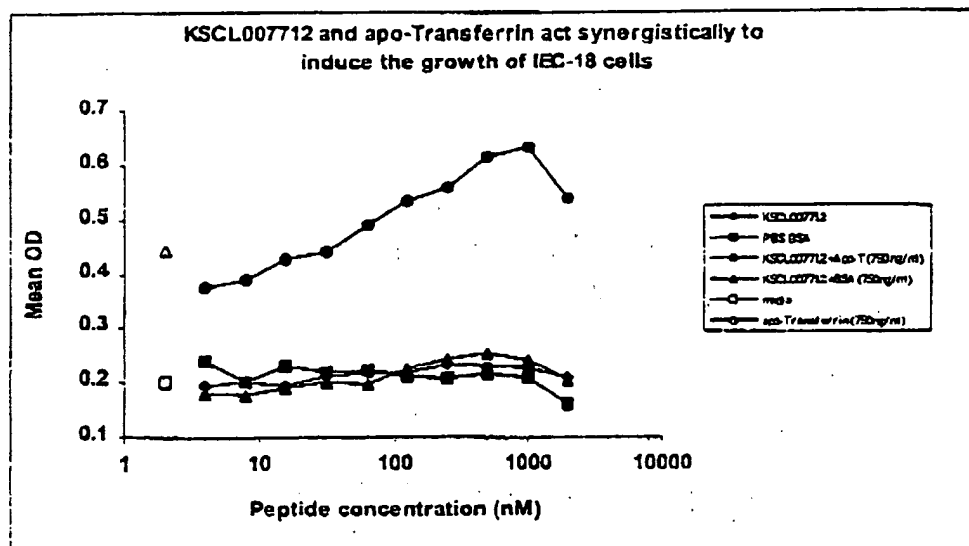
6/16

Figure 6



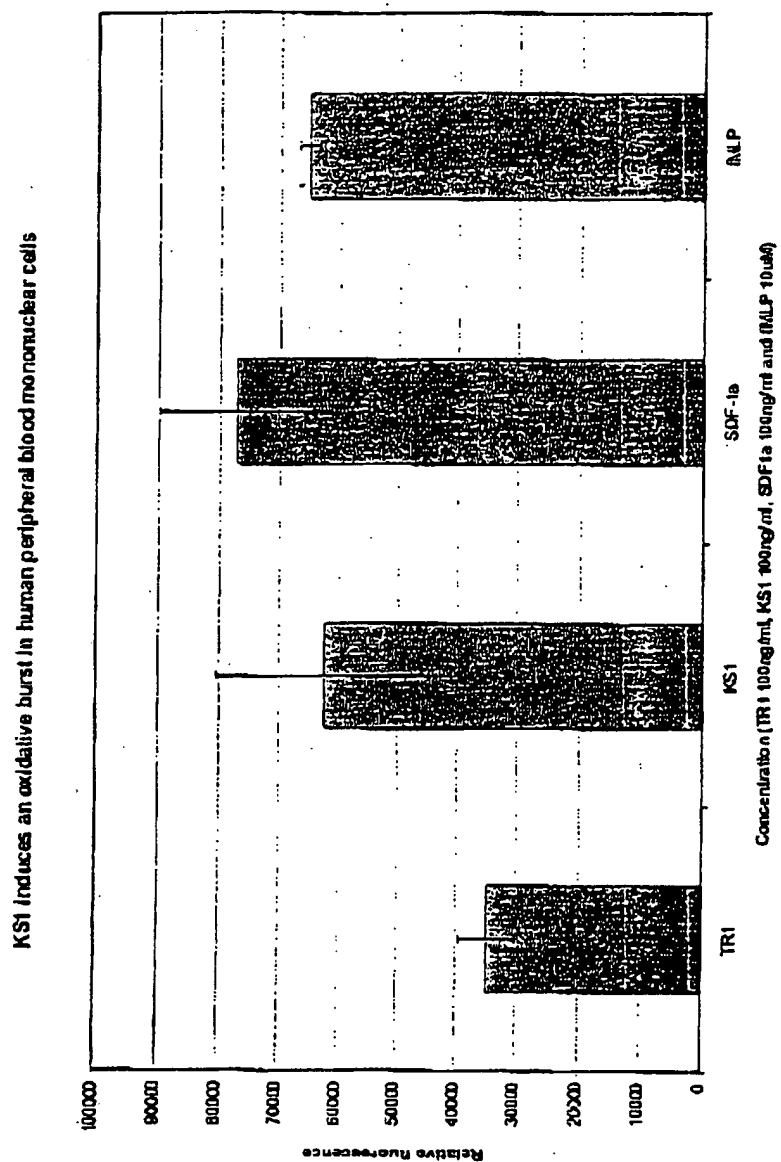
7/16

Figure 7



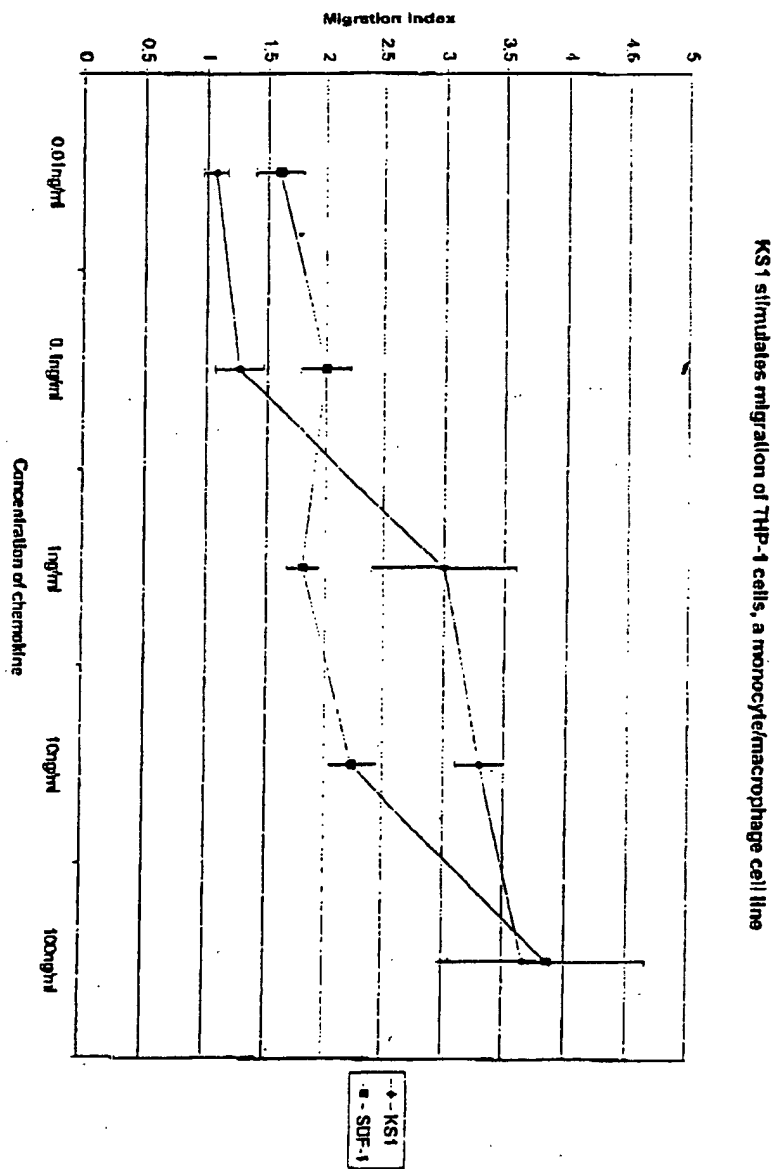
8/16

Figure 8



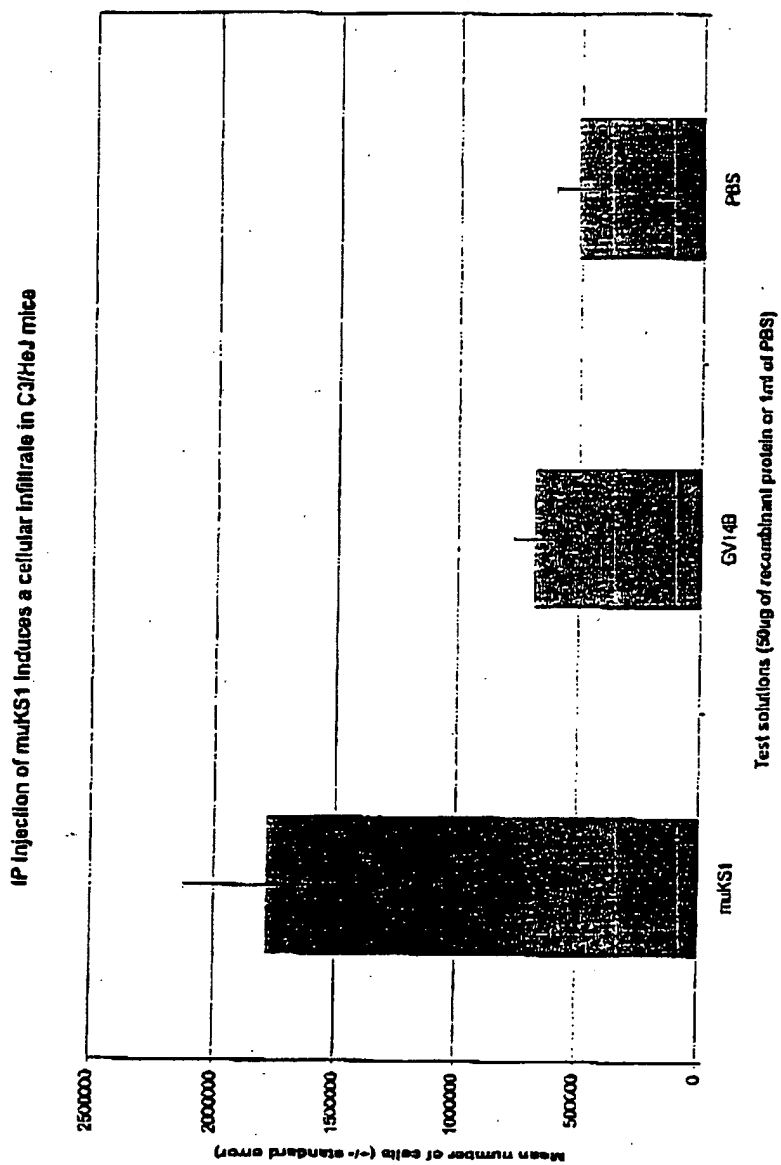
9/16

Figure 9



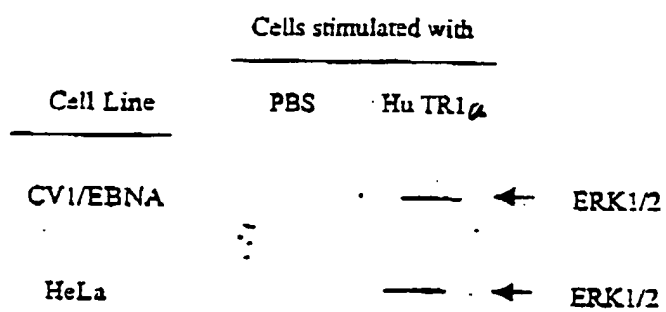
10/16

Figure 10



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Figure 11



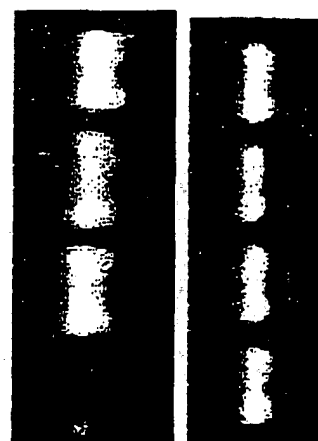
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Figure 12

mu and huTR1 upregulate huTR1 mRNA expression in HeLa cells

HeLa cells stimulated with

PBS muTR1 huTR1 huTGF α



huTR1 mRNA

Actin mRNA

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Figure 13A

Murine Tr1 activates the SRE reporter in PC12SRE cells

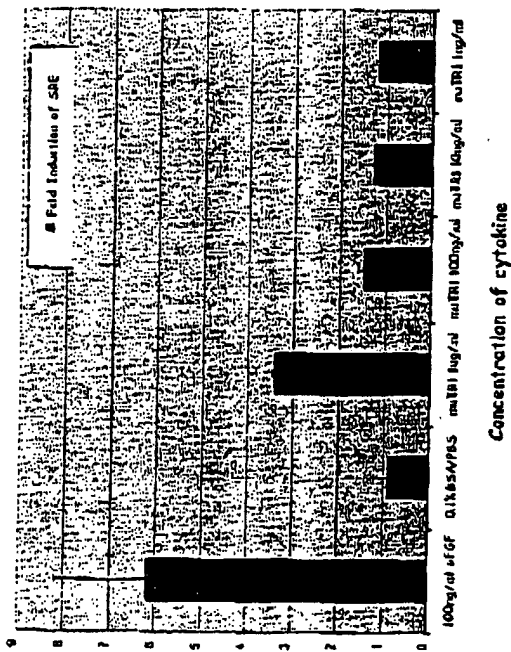
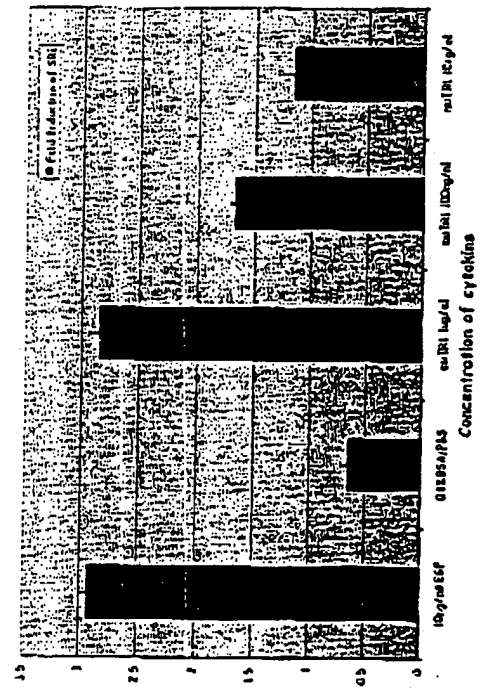


Figure 13B

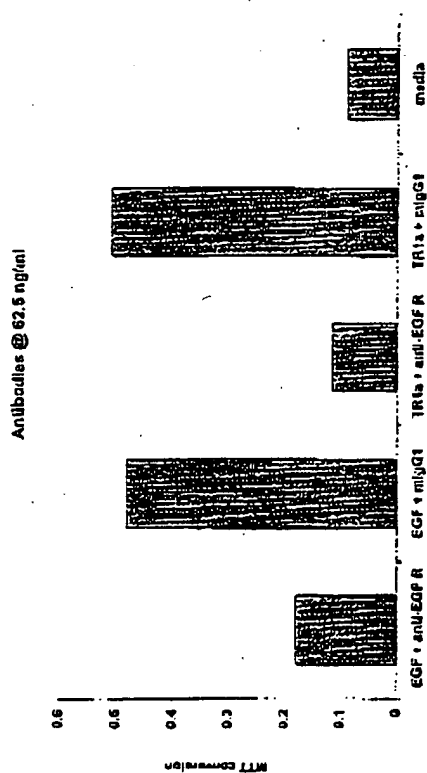
Murine Tr1 activates the SRE reporter in HoesatSRE cells



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Figure 14

TR1 growth of HaCat cells is inhibited by an antibody to the EGF receptor



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Figure 15a

-202 GC
 -200 AGCACCCAGC GCCAAGCGCA CCAGGCACCG CGACAGACCG CAGGAGCACC
 -150 CATCGACGGG CGTACTGGAG CGAGCCGAGC ACAGCAGAGA GAGGCGTGCT
 -100 TGAAACCGAG AACCAAGCCG GCGGCGATCC CCCGGCCGCC GCACGCACAG
 -50 GCCGGCGCCC TCCTTGCCCTC CCGCTCCCC ACCGCGCCCC TCCGGCCAGC

1 ATG AGG CTC CTG GCG GCC GCG CTG CTC CTG CTG CTC CTG GCG
 1 M R L L A A A L L L L L L A

43 CTG TGC GCC TCG CGC GTG GAC GGG TCC AAG TGT AAG TGT TCC
 15 L C A S R V D G S K C K C S

85 CGG AAG GGG CCC AAG ATC CGC TAC AGC GAC GTG AAG AAG CTG
 29 R K G P K I R Y S D V K K L

127 GAA ATG AAG CCA AAG TAC CCA CAC TGC GAG GAG AAG ATG GTT
 43 E M K P K Y P H C E E K M V

167 ATC GTC ACC ACC AAG AGC ATG TCC AGG TAC CGG GGC CAG GAG
 57 I V T T K S M S R Y R G Q E

211 CAC TGC CTG CAC CCT AAG CTG CAG AGC ACC AAA CGC TTC ATC
 71 H C L H P K L Q S T K R F I

253 AAG TGG TAC AAT GCC TGG AAC GAG AAG CGC AGG GTC TAC GAA
 85 K W Y N A W N E K R R V Y E

295 GAA TAG GGTGGACGAT CATGGAAAGA AAAACTCCAG GCCAGTTGAG AGA
 98 E ***

344 CTTCAGC AGAGGACTTT GCAGATTAAA ATAAAAGCCC TTTCTTTCTC ACA
 394 AGCATAA GACAAATTAT ATATTGCTAT GAAGCTCTTC TTACCAGGGT CAG
 444 TTTTATAC ATTTTATAGC TGTGTGTGAA AGGCTTCCAG ATGTGAGATC CAG
 494 CTCGCCT GCGCACCAGA CTTTATTACA AGTGGCTTTT TGCTGGGCGG TTG
 544 GCGGGGG GCGGGGGGAC CTCAAGCCTT TCCTTTTAA AATAAGGGGT TTT
 594 GTATTTG TCCATATGTC ACCACACATC TGAGCTTTAT AAGCGCCTGG GAG
 644 GAACAGT GAGCATGGTT GAGACCGTTC ACAGCACTAC TGCTCCGCTC CAG
 694 GCTTACA AAGCTTCCGC TCAGAGAGCC TGGCGGCTCT GTGCAGCTGC CAC
 744 AGGCTCT CCTGGGCTTA TGA CTGGTCA GAGTTTCAGT GTGACTCCAC TGT
 794 GGCCCT GTTGCAGGGC AATTGGGAGC AGGTCCTTCT ACATCTGTGC CTA
 844 GAGGAAC TCAGTCTACT TACCAGAAGG AGCTTCATCC CCACCCACC CCC
 894 ACCCGCA CCCAGCTCA TTCCCTGTC ACGACCAGGC AAGTGATCCT TAA
 944 AGGACCT GGGTCTTTTT CTGCAAACT GAGGGTTTCT GAAAGGTGG CTG
 994 CTTTGGT AGAAGATGCT TCTGAGGCAT CCAAAGTCCC CAGCAGTGTG AGA
 1044 AAATGAT TCTCGATGTT CCGGAGGACA AGGGAAGATG CAGGATTAGA TGC
 1094 AGGACAC ACAGCCAGAG CTACACATCC TCTTGGCAAT GGGAGCTCCC CCC
 1144 CCCCAA GCTTTGTTTC TTTCCCTCAC CCCAACAGAA AGTGCACTCC CCC
 1194 TCAGTGA ATACGCAAC AGCACTGTTC TCTGAGTTAG GATGTTAGGA CGA
 1244 TCCTGCG CCCTGCCCTC TCCTGTGTAC ATATTGCCTT CAGTACCCCT CCC
 1294 CCACCCC ATGCCACACA CTGCCCTCA TTAGAGGCCG CACTGTATGG CTG
 1344 TGTATCT GCTATGTAAA TGCTGAGACC CCGAGTGCT GCATGCAGGT TTC
 1394 ATGTTCT TTCTAAGATG AAAAGAGAAA GTAATAAAAT ATATTGAAG TTC
 1444 CCCAAA AAAAAAAAAA A

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Figure 15b

KLF-1M	RLAAAA...L	LLLLLALCAS	RVDGS.....	.K CKCSRKG
BRAKM	RLPAAA...L	LLLLLLALYTA	RVDGS.....	.KCKCSRKG
mCrg-2	MNPAAVIFC	LILLGLSGTQ	GIPLAR....	TVRCNCIHID
mMig	MKSAVLFLG	IIFLEQCGVR	GTLVIR....	NARCSCISTS
mSDF-1	MDAKVVAVLA	LVLAALCISD	GKPVSL....	.YRCPCRFFE
mBLCM	RLSTAT...L	LLLLASCLSP	GHGILEAHYT	NLKCRCSGVI
mMIP-2M	AP....PTC	RLLSAALVLL	LLLATNHQAT	GAVVAS....
mKCM	IP....ATR	SLLCAA...L	LLLATSRLAT	GAPIAN....
mLix	MSLQLRSSAH	IPSGSSSPFM	RMAPLA.FLL	LFTLPQHLAE	AAPSSVIAAT
					ELRCQCLQTM
					ELRCVCLTVI

Consensus

C C

KLF-1	.PK.IRYSDVK	KLEMKPKYPH	CEEKMVIIVTT	KSMSRYRGQE	HCLHPKLQST	KRFI....KW
BRAK	.PK.IRYSDVK	KLEMKPKYPH	CEEKMVIITT	KSVSRYRGQE	HCLHPKLQST	KRFI....KW
mCrg-2	DGPVRMRAIG	KLEIIPASLS	CPRVEIIATM	KK....NDEQ	RCLNPESKTI	KQLM....KA
mMig	RGTIHYKSLK	DLKQFAPSPN	CNKTEIATL	K....NGDQ	TCLDPDSANV	KKLMKEWEKK
mSDF-1	SH.IARANVK	HLKILN.TPN	CALQIVARLK	N....NNRQ	VCIDPKLKIWI	QEYL...EKA
mBLC	STVVGLNIID	RIQVTPPGNG	CPKTEVVIWT	K....MKKV	ICVNPRAKWL	QRLLRHVQSK
mMIP-2	PR.VDFKNIQ	SLSVTTPGPH	CAQTEVIATL	K....GGQK	VCLDPEAPLV	QKII....QK
mKC	AG.IHLKNIQ	SLKVLPSGPH	CTQTEVIATL	K....NGRE	ACLDPEAPLV	QKIV....QK
mLix	PK.INPKLIA	NLEVIPAGPQ	CPTVEVIAKL	K....NQKE	VCLDPEAPVI	KKII....QK

Consensus

C

C

KLF-1	YNAWNE.KRR	VYEE.....
BRAK	YNAWNE.KRR	VYEE.....
mCrg-2	FSQKRS.KRA	P.....
mMig	INQKKKQKRG	KKHQKNMKQR	KPKTPQSRRR SRKTT
mSDF-1	LNKRLKM...
mBLC	SLSSTPQAPV	SKRRAA....
mMIP-2	ILNKGK.AN.
mKC	MLKGVP.K..
mLix	ILGSDK.KKA	KRNALAVERT	ASVQ.....

Consensus

1011c2PCTSEQUENCE LISTING

SEQUENCE LISTING

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Watson, James D.
 Strachan, Lorna
 Sleeman, Matthew
 Onrust, Rene
 Murison, James G.
 Kumble, Krishanand D.

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 and methods for their use

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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<400> 16

1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

<220>

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1011c2PCTSEQUENCE LISTING

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 <213> mouse

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1011c2PCTSEQUENCE LISTING

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<212> DNA
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<400> 24

1011c2PCTSEQUENCE LISTING

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 <213> Rat

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
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1011c2PCTSEQUENCE LISTING

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<212> DNA
<213> Rat

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Rat

<400> 29

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 <212> DNA
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<220>

<400> 30

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1011c2PCTSEQUENCE LISTING

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<210> 32
 <211> 434
 <212> DNA
 <213> mouse

<400> 32

1011c2PCTSEQUENCE LISTING

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 903

1011c2PCTSEQUENCE LISTING

<210> 34
 <211> 1359
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (644) ... (644)

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 360
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 420
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 960
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 1260
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1011c2PCTSEQUENCE LISTING

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1359

<210> 35
<211> 797
<212> DNA
<213> mouse

<400> 35
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240
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300
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360
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420
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480
gaaaatggac attcctttcc ttggtgaaat gccccagag gatgggatgt agagaaggga
540
aaccctagcg gaatccaacc agacttactc atctcactga cggcacccaa gaagtctgca
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660
aagaagtacc agctgaacct gccatcttac cctgacacag agtgtgtcta ccgtctacag
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780
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797

<210> 36
<211> 896
<212> DNA
<213> mouse

<400> 36
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120
cccatcccgag atttgcttag tttgtctccc aatgtgctgg actttaaaga cagggaatgg
180
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240
tgtacctgtc cttggctgga ccctgggcag taactgtcac tcagatgagg acgatcatca
300
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1011c2PCTSEQUENCE LISTING

360
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480
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720
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780
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896

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<211> 501
<212> DNA
<213> mouse

<400> 37
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180
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<210> 38
<211> 766
<212> DNA
<213> mouse

<400> 38
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120

1011c2PCTSEQUENCE LISTING

cgggcggcat cccccggccg ccgcacgcac aggcggcgcc cctccttgcc tccctgctcc
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 480
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 766

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 <211> 480
 <212> DNA
 <213> mouse

<400> 39
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 aatcattctc acatgcttcc atgtttgttt ctgagagggt ggggctcaaa tgtatagaaa
 240
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 420
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 480

<210> 40
 <211> 962
 <212> DNA
 <213> mouse

<400> 40
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1011c2PCTSEQUENCE LISTING

120
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 180
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 240
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 420
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 480
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 720
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 780
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 840
 aatgagtggg ttgcagtgaag agccaggcat cctgtagttt ccatcccctc ccccatccca
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 960
 aa
 962

<210> 41
 <211> 794
 <212> DNA
 <213> mouse

<400> 41
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 240
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 420
 attaccccaa aagacctaac aagcccctct tcaactgggt agtgactcag tgtcagaaaa
 480
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1011c2PCTSEQUENCE LISTING

540
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660
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720
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780
aaaaaaaaact cgag
794

<210> 42
<211> 1152
<212> DNA
<213> mouse

<400> 42
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120
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240
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480
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660
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720
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1020
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1011c2PCTSEQUENCE LISTING

1140
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1152

<210> 43
<211> 446
<212> DNA
<213> mouse

<400> 43
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446

<210> 44
<211> 391
<212> DNA
<213> mouse

<400> 44
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391

<210> 45
<211> 516
<212> DNA
<213> Rat

<400> 45
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1011c2PCTSEQUENCE LISTING

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 300
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 420
 cagcgaggtc cctgacaggg cacctgacag cccgcaggaa gagggcctgg acttcttcca
 480
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 516

<210> 46
 <211> 306
 <212> DNA
 <213> mouse

<400> 46
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 180
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 306

<210> 47
 <211> 439
 <212> DNA
 <213> mouse

<400> 47
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 gcacatatta ctgagccatt gcaagcaatg ggaggggtcc acaatgacac acacacacac
 180
 acacacacac atacacatac acacaccccc gagacagtgc cagagctaac agcctacatg
 240
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 300
 ttgcaagtga tcttccatgc agtatgaaac atgcagacag cactggagtg tggcaagagt
 360

1011c2PCTSEQUENCE LISTING

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 439

<210> 48
 <211> 159
 <212> DNA
 <213> mouse

 <220>
 <221> unsure
 <222> (3)...(3)

<400> 48
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 159

<210> 49
 <211> 465
 <212> DNA
 <213> Rat

<400> 49
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 120
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 180
 attggcatgt ttcttggtgg cttgggtgcc accatcttcc tggacattat ctacattagc
 240
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 300
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 360
 gagggggtga gctcccgtc cgctcggatt tcttcggacc ttctcaggaa catagtgcct
 420
 accagacaat tgactcgtca gactcacctg cagaccccct tgcaa
 465

<210> 50
 <211> 337
 <212> DNA
 <213> Rat

<220>

<400> 50
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1011c2PCTSEQUENCE LISTING

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<210> 51
 <211> 371
 <212> DNA
 <213> Rat

<220>
 <221> unsure
 <222> (80)...(80)

<221> unsure
 <222> (312)...(312)

<221> unsure
 <222> (319)...(319)

<221> unsure
 <222> (353)...(354)

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 tgcccattct t
 371

<210> 52
 <211> 228
 <212> DNA
 <213> Rat

<400> 52
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1011c2PCTSEQUENCE LISTING

120
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 228

<210> 53
 <211> 361
 <212> DNA
 <213> Human

<400> 53
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 240
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 360
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 361

<210> 54
 <211> 403
 <212> DNA
 <213> Human

<220>

<400> 54
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 ttggcgatcc tgttgtgctc cctggcattg ggcagtgtta cagtgcactc ttctgaacct
 180
 gaagtcagaa ttcctgagaa taatcctgtg aagttgtcct gtgcctactc gggcttttct
 240
 tctccccgtg tggagtggaa gtttgaccaa ggagacacca ccagactcgt ttgctataat
 300
 aacaagatca cagcttccta tgaggaccgg gtgaccttct tgccaactgg tatcaccttc
 360
 aagtcctgta cacgggaaga cactgggaca tacacttgta tgg
 403

<210> 55
 <211> 413
 <212> DNA
 <213> Human

1011c2PCTSEQUENCE LISTING

<400> 55
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120
tgggcatgaa gtgcacgcgc tgtgggggag acgacaaagt gaagaaggcc cgtatagcca
180
tgggtggagg cataattttc atcgtggcag gtcttgccgc cttggtagct tgctcctggt
240
atggccatca gattgtcaca gacttttata accctttgat ccctaccaac attaagtatg
300
agtttggccc tgccatcttt attggctggg cagggctctgc cctagtcatc ctgggagggtg
360
cactgtctcc tgttctctgc ctggggataa gagcagggtt gggtagctgc ccg
413

<210> 56
<211> 452
<212> DNA
<213> Human

<400> 56
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180
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300
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360
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420
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452

<210> 57
<211> 190
<212> DNA
<213> Rat

<220>

<400> 57
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180
gcgtattcgg
190

1011c2PCTSEQUENCE LISTING

<210> 58
 <211> 413
 <212> DNA
 <213> mouse

<400> 58
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 120
 tttttccac ctgctgccct cacctgagcc cagcccagag ggcagctacg tgggccagca
 180
 ctcccagggc ctcggcgggc actacgcgga ctctacctg aagcggaaga ggattttcta
 240
 aggggtcgac accagagatg ctccaagggc ctgcaccaag ttgcttttgg gttttttctg
 300
 gtatttgtgt tttctgggat tttattttta ttattttttt taatgtcctt tctttgggta
 360
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 413

<210> 59
 <211> 325
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (213)... (213)

<221> unsure
 <222> (223)... (223)

<221> unsure
 <222> (227)... (227)

<221> unsure
 <222> (243)... (243)

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 120
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 180
 tcttgggtga ccaacatctt cctgtctttg agnaaccagg ggcagnatg ggagccaccc
 240
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 300
 agagagggag tgaagaaagg ggcca
 325

<210> 60

1011c2PCTSEQUENCE LISTING

<211> 372
 <212> DNA
 <213> mouse

<400> 60
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 120
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 180
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 240
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 300
 cgcacacaaa ggacatgtgg ctacgcgtgg ccaagttcct tcccgaaaga acctgcactt
 360
 tggctgtgtg ga
 372

<210> 61
 <211> 363
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (15)...(15)

<400> 61
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 120
 ccaagagctt tccaccaaag aagccctcc aagcactgac catgtctatt atggaccaca
 180
 gccccaccac cggggtggta acggtcattg tcatcctcat cgccatagct gccctggggg
 240
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 360
 taa
 363

<210> 62
 <211> 399
 <212> DNA
 <213> mouse

<400> 62
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 120

1011c2PCTSEQUENCE LISTING

ctctccaaca tctcgccat caccgacctc ggtggctttg acccagtgtg gcttttcctc
 180
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 240
 gagagacatt aattaaacac tccctcacc caccgcacca aaccagttgg gttcttctga
 300
 tattctggaa tactctgggc tatgttttat gtttatttct tttttaatcg gttgtatttt
 360
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 399

<210> 63
 <211> 399
 <212> DNA
 <213> mouse

<220>

<400> 63
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 120
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 180
 cagagcacct ggtctataat cacacaacct agcctctctg agcctgggac tcttgccagt
 240
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 300
 tcttcttacc tctttcctgg gcatacttac gctgtctcag aagacagatc tctgggcctc
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 399

<210> 64
 <211> 2481
 <212> DNA
 <213> Rat

<400> 64
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 120
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 180
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 240
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 420
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1011c2PCTSEQUENCE LISTING

480
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 600
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 660
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 720
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 780
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 1200
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 1260
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 1320
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 1380
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 1440
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 1680
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 1740
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 1800
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 1860
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 1920
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 1980
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 2040
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 2100

1011c2PCTSEQUENCE LISTING

ataagggatt attaccaaag cagcagggtg cgctgcctgt caaacgacta gaagtatctc
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 2220
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 2280
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 2481

<210> 65
 <211> 3008
 <212> DNA
 <213> mouse

<220>

<400> 65

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 240
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 420
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 480
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1011c2PCTSEQUENCE LISTING

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 1140
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 1200
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 2580
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 2640

1011c2PCTSEQUENCE LISTING

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 3000
 aaaaaaaa
 3008

<210> 66
 <211> 1888
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (1690)... (1690)

<221> unsure
 <222> (1755)... (1755)

<221> unsure
 <222> (1864)... (1864)

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 600
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 660
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 720

1011c2PCTSEQUENCE LISTING

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 900
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 960
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 1020
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 1080
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 1140
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 1380
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 1680
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 1740
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 1860
 accngtggct cgcattctca ttgacctg
 1888

<210> 67
 <211> 1260
 <212> DNA
 <213> Rat

<400> 67
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 120
 acacctgctc ctgcactgat gggactggc ttctggaagg gcagtgccta gatattgatg
 180
 aatgtcgcta tggttactgc cagcagctct gtgcgaatgt tcctggatcc tattcctgta
 240

1011c2PCTSEQUENCE LISTING

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 300
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 360
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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Rat

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1011c2PCTSEQUENCE LISTING

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<212> DNA
<213> Human

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1011c2PCTSEQUENCE LISTING

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<212> DNA
<213> mouse

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<212> DNA
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<400> 73

1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

1633

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 <212> DNA
 <213> mouse

<400> 74

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 <212> DNA
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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> mouse

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> mouse

<220>

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<210> 78
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 <212> DNA

1011c2PCTSEQUENCE LISTING

<213> mouse

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<210> 79

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<212> DNA

<213> mouse

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<400> 79

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<210> 80

<211> 214

<212> DNA

<213> mouse

<400> 80

cccagaccct gtgtcagcta tcccagcaga aaaagaagat gcggaccctc tcagcaagtc
60
aggtgaggaa acccaggaag cagggtcattg accccgcaga ggtcggggct cctgggtgcag
120
aggatcagat cttgtgtgac ttctgtcttg gggccagcag agtaagggca gtgaaatcct
180
gtctgacctg catggtgaaa tactgtaagg agca
214

<210> 81

<211> 152

<212> DNA

<213> mouse

<220>

1011c2PCTSEQUENCE LISTING

<400> 81

ccccttaact aaccaggac cttccactaa gtggaaggct ccaccatcca cagagggggc
60
cagtcatttt taagcacacg gaccttttgt gagacagtcg tgatcttaac tgtgggtgtca
120
ctgatggagc tgaacgggat cccctaaaag ta
152

<210> 82

<211> 181

<212> DNA

<213> mouse

<220>

<400> 82

tctcagtgat gatgagaagc tccggaggag gcaggagaaa gcagggcccc gccctccct
60
gggtctccac ccaccacgc ccgctaaggc cacctgttct cccatggaga tgatgaagaa
120
gctcatagct ggacaaggcc cggaacctca gcccagtaac cgacctactt cccgcctggg
180

a

181

<210> 83

<211> 332

<212> DNA

<213> mouse

<220>

<400> 83

tatagagatg gtgatgtaat gggccagggt gtaagcttca acctggggga ttttgctggt
60
tttggtgttt ccctgtgtag ccctaacaag cctgtgtaga ccaggctggc ttttaactttg
120
cagatgacat tcacgtctac ttctctctgt gttgggggta tgggtctgca cacctgcca
180
ggcctaggct gggggatttt gaagtatctt agattatgga gtagaccag agtttgcaag
240
tatctgcttt aaagtgcac ataaacatag cctcctgacc atcttccaca gtgggaccct
300
gatctggcct ctccctggaa gaagagagaa ag
332

<210> 84

<211> 213

<212> DNA

<213> mouse

<400> 84

gcaggcagat aacaatgatt actggacaga gtgcttcaac gcattggaac aggggaggca

1011c2PCTSEQUENCE LISTING

60
 atatgtggat aatccacacag gcgggaaagt ggacgaggct ctggtgagaa gtgccaccgt
 120
 acattgttgg ccgcacagca acgtgctgga cacaagcatg ctctcatccc cagatgtggt
 180
 gcgcatgctg ctgtccctgc agcccttcct gca
 213

<210> 85
 <211> 273
 <212> DNA
 <213> mouse

<220>

<400> 85
 ccggctctct ctctcctcct tccccgcctc ttctgcctcc cctgcctgga actctgatga
 60
 ggagggaacca ggtggtcagg caccacagtc tgatcaggac tcctgtggcc tccagagttt
 120
 cactcccccg tccatcctga agcgggctcc tcgggagcgt ccagggtcacg tggcctttaa
 180
 cggcatcacc gtctactatt tccacagggt ccagggatcc accagtgtgc ccagccgtg
 240
 gtggctgtac cctgggcatg gcttctcggc aca
 273

<210> 86
 <211> 218
 <212> DNA
 <213> mouse

<400> 86
 ctcagccgcc tgctctgggg gctggagggt ctccactta actgtgtctg ccgttcaggg
 60
 ggctcaccga gtgctgcgct acacagaggt tttccctcca gctccagtcc gtccctgccta
 120
 ctcttctat aaccgcctcc aagagctggc ctactgttg ccccgcccg ataagccctg
 180
 ccagcctat gtggagccta tgactgtggt ttgtcacc
 218

<210> 87
 <211> 335
 <212> DNA
 <213> mouse

<400> 87
 gaggtgggggt ggggtgcatag cctgcctgca attgctgccg ctgggcttaa cgtgttgtga
 60
 gctggccggt ttcctacaca gcagcacctg ccatggagcc tggccacaag gccactcaga
 120
 gctgggtgga cagagtgtga ccagaaactc cctgtggggt ctgataaagg attctcccat
 180

1011c2PCTSEQUENCE LISTING

aggcaagggtt cagagaacct gggcctcctg ttctcaggga ggctgtcta tccccagcct
 240
 ctgagctggt tcgtcctagt tggtagagta agtggcatag ccctcttgag gcctctgatg
 300
 tggaaggggc acagaattgc aattattctt gcatg
 335

<210> 88
 <211> 410
 <212> DNA
 <213> mouse

<400> 88
 aaaccccgcc aggaaacaaa taccgggtgta tcggctttac tgaatgcatt tattcccaaa
 60
 gggaaactga aaagcaacct agggacactg taagcagaaa gctgaggctt ttaaaaaccc
 120
 accttggcaa tgtaacttgg gaggttccca cacaccagg gctgtgcac gtgaaattct
 180
 gtctcctgag acgctgagaa acccttcctt gcagctataa tgggcctggc cgcccagtgt
 240
 ggagctgtag cttcccacga cgtagccctc aggaacttca ggagggatgc cacagtctat
 300
 ttctgaaaac aaaaccgtgt caacttcttt actttacaaa tgcaagtttt cagaatccac
 360
 catctctctg cacccatacc ccatgcctca cccccagac cctgtgttag
 410

<210> 89
 <211> 279
 <212> DNA
 <213> mouse

<220>

<400> 89
 gtgcagagag tggattgtca gtggactgct cagttacaaa tgggacatct aacacacaca
 60
 cacacacaca cacacacaca cacacacaca ccccccaagg cttagagacc attgcagaag
 120
 agaagagttt atgggaaatc ttggagaaaa cattggatgg tttgagagaa tggttaggag
 180
 atcagactag ctagtccagg aagcagtga ggggggcggg gttagaagat gaggtcagaa
 240
 gacagggtgg agggcattgt ccgacagaac cattgctgt
 279

<210> 90
 <211> 398
 <212> DNA
 <213> mouse

<400> 90
 ccaccaaccc agaaatttga caaaggggtt gaatgttga ctttgcgtcc tccccggca

1011c2PCTSEQUENCE LISTING

60
 gtggatgtac tgttttgagc cctgtgtgga acttctgaac ttcgtgctgt aactttcaga
 120
 actcttagac atgggtgtgc tcaactgaact ctagggtctg tgtgctagat gctgccaacg
 180
 ctgtattcag gacctgaagt gagtaccctg gtggatccag accaatccag tgtgagacta
 240
 ctgaagaaca tctgttgcca gaacggccac accaaacaga tggagtgtcc cagcacttag
 300
 cttcttaa at aacatcgga ccattcagcc agcgagtctg tgtttgcttt ttgttaaatt
 360
 gtccgccgaa tctaaattcc tccaaaaggc ttgtgacc
 398

<210> 91
 <211> 279
 <212> DNA
 <213> mouse

<400> 91
 gttgttactt cagttgctct cggcgggaat tcttaaactg catcctgagt gagggagctt
 60
 tggcgagaaa gcaagaccca gtggtagaca gattagcatt actgtacagc ttctttgggt
 120
 gttcgaggaa gcccggtgg accatagtgg ccacggcggg gaggtaggcg tggacagggc
 180
 tgaccagtcc aagttaagga cgttcgggtc catgttaacc ctgccttgta cgtccagcat
 240
 cgtaagaaaa aacacttgag aaccggaaga ggagatgga
 279

<210> 92
 <211> 401
 <212> DNA
 <213> mouse

<400> 92
 aaaaagtttt accaaaacct tttattgact tttataaatt agatagtatt tcaaagttta
 60
 tgtagaatcg tattctttga aactgtactt agcagagcag aagaggcctg ctgacgctag
 120
 cagctctgc aatgaatcat gtggcaccga gtctacgcca agggccccga gaaactttat
 180
 tccatagatg ggcagatggg tcccaaagtt acactacaga actacaaatc gactcttaaa
 240
 attaaaacgg gactttacaa gcattctaga agactcaaac ttgaagcaat ttttggaaaa
 300
 taaatgtaca gagaaaagat cttgaagcta ctgaacagag aaccctcatt aaccgagcaa
 360
 atacatccta tggagcttcc gaggagtaca cagacagacc g
 401

<210> 93
 <211> 339
 <212> DNA

1011c2PCTSEQUENCE LISTING

<213> mouse

<400> 93

ccactgacct tcccagaagg tgacagccgg cggcggatgt tgtcaaggag ccgagatagt
60
ccagcagtgc ctcggtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg
120
atgagaagtc accacagtga tctcacattt tgcgagatta tctgatgga gatggagtcc
180
catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataccga
240
cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg
300
tacactagct cagaagagtt tgcagctgat gctctgctg
339

<210> 94

<211> 55

<212> DNA

<213> mouse

<400> 94

ggggtgtggg caacttggat aacctcagct gcttccatct ggctgacatc tttgg
55

<210> 95

<211> 186

<212> DNA

<213> mouse

<400> 95

ggactctggc ttcctggggc tgcggccgac ctcggtggat cccgctctga ggcgggcggcg
60
gcggggcccc agaaacaaga agcgcggtcg gaggaggctc gccgaggagc cgctgggggtt
120
agaggtcgac cagttcctgg aagacgtccg gctacaggag cgcacgaccg gtggcttggt
180
ggcaga
186

<210> 96

<211> 244

<212> DNA

<213> mouse

<400> 96

ggtgacaaa accccttctg ccccttccc agagactctg acttgaccct ctttccaatt
60
ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggccc
120
aagagggcat gaggcacacc ctgatcactg tctcaggcct ttgtgggcac tgactcgacc
180
ctggcccacc tcacgcccc aggccagttg gcaactggtg gctcttgagg gctcttacgc
240
cctt

1011c2PCTSEQUENCE LISTING

244

<210> 97
 <211> 116
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (11)...(11)

<221> unsure
 <222> (13)...(13)

<221> unsure
 <222> (41)...(41)

<400> 97
 acccggtctg ngnactgccc gccttctggg gcttccttta naggatacag tcttttaccc
 60
 atctaggact cctgccaccc tgactgctga cttacagcta tgaggccccg gcttct
 116

<210> 98
 <211> 307
 <212> DNA
 <213> mouse

<400> 98
 ccccgggcca tctgtcgcca taccggggccc gtgcaagctt ttgcaggttt tagaagatgg
 60
 cgaattcatg acacctgtga tccaggacaa cccctcaggc tggggtcctt gtgccgttcc
 120
 tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaaggt
 180
 tgcagactgg acagggggcca cataccagga caagaggtag acaacaagt attcctctca
 240
 gttcgggtggg gggagtcagt atgcatatct ccatgaggag gatgagacaa gctttccagc
 300
 tgggtgg
 307

<210> 99
 <211> 360
 <212> DNA
 <213> mouse

<220>

<400> 99
 ccttgggtgca ccagctccag cctcaggact tcctcctcct ggccctgaca gccagctct
 60
 tgtcccagca gaatccagt acaggaagga gtttctgagg caggggagga ggcttctcca
 120

1011c2PCTSEQUENCE LISTING

tgggaaccag acagccttgc ttcactgtat aagtgccctg atcacacgca gaatgaagtg
180
ccagggttgc cagaagcaca aaggggtgtg ctactggccc taaccatgga ctacgtggtt
240
ctaaccaaag actctagaac tctgggggtg gggagaaaca atgtgttctg tgctccagaa
300
ctcggctt cctggcccat atggatgggc ttggcaagga acctacctct tctctaaggt
360

<210> 100
<211> 257
<212> DNA
<213> mouse

<400> 100
tgccgcgctg agaggggggg cgcaccacc agcgccacca ccaccaccgc cgccgcccgc
60
gggtgggggtg ggagggggcg gagccaccgc taccgccgcc gcctcccggg tgggcgccct
120
tctccttaga cgccggcgac ccaggacgag ggcttcatca ctgtaaatgg ttgcaagccg
180
acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg
240
gacgcatttc tatcggg
257

<210> 101
<211> 203
<212> DNA
<213> mouse

<400> 101
ccaaagtgcc cattgtgatt caagacgata gccttcccac ggggccccct ccacagatcc
60
gcatectcaa gaggcccacc agcaacggtg tggtcagcag ccccaactcc accagcaggc
120
cagcccttcc tgtcaagtcc ctagcacagc gggaggcaga gtatgcagag gctcggagac
180
ggatcctagg cagtgccagc cct
203

<210> 102
<211> 300
<212> DNA
<213> mouse

<400> 102
agtacagaga cctcggctgc agcttaaacc tcggacagtg gcaacgcccc tcaatcaagt
60
agccaacccc aactcagcca tctttggggg agccaggccc agagaggaag tggttcagaa
120
ggagcaagaa tgagcttagg ttgggaggga atggggcgtg ggggagctgg agcaagacca
180
cggcctgggtg gcagccggtc gccctacagg cccattccc gcctggcact gtccctccta
240

1011c2PCTSEQUENCE LISTING

cagcggaaac acagagcttg tgagtgcattg tcagctgtta acaagtgggt tctagtacat
300

<210> 103
<211> 370
<212> DNA
<213> mouse

<220>

<400> 103
cagcaactgt ttcaggagct gcacgggtgta cgcttgctga ctgatgcgct ggaactaaca
60
ctgggagctgg cccccaaga aaaccctccg gtgatgcttc cagccaaga gacggagagg
120
gccatggaga tcctcaaagt gctctttaat atcaccttg actctgtcaa gagggaggtt
180
gatgaggaag atgctgccct ttaccgggtac ctggggactc ttctgcggca ctgctgatg
240
gttgaagctg ctggggaccg cacagaggag ttccacggcc acacggtgaa tctcctgggg
300
aacttgcccc tcaagtgttt ggatgtgctt ctggccctgg agctccacga aggatcctta
360
gagtcaatgg
370

<210> 104
<211> 423
<212> DNA
<213> mouse

<400> 104
tttcccagcc tggtaggagca gccgactggc gagggtgcca actgtcccgt gcttcccagc
60
tcctaccttg cctgtcttct ctctcctggg aagatgttcc tggtaggggt gacgggaggc
120
atgcctcag gcaagagctc cgtcatccag gtattccaac agctgggctg tgctgtaatc
180
gacgtggacg tcattgcgag gcacgttgct cagccagggt atcctgcccc ccggcgata
240
gtagaggcct ttggcactga agtcttgctg gagaatggcg acatcgaccg caaggctctc
300
ggagacctga tcttcaacca gcctgaccgt cggcagctgc tcaactccat taccaccct
360
gagatccgca aggaaatgat gaaggagacc ttcaagtact tctccgaggt accgatacgt
420
gat
423

<210> 105
<211> 117
<212> DNA
<213> mouse

1011c2PCTSEQUENCE LISTING

<400> 105
 agcttggtgc tgttcatatt taaactgata aagactcttc ataggagctg agggtagcaa
 60
 gcccgcgctcg gtgactgggg tctcacacag gttcagcact tggagcatag tgaggtg
 117

<210> 106
 <211> 133
 <212> DNA
 <213> mouse

<400> 106
 tttttttttt aaaataccac catttccaat cccaaaagaa catggcactt gtttgtttct
 60
 tccccttctc attcattcca gactttcaag tgttttcttc aatactgagg ctttctcctg
 120
 cagctctggt ctg
 133

<210> 107
 <211> 217
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (1)...(1)

<221> unsure
 <222> (11)...(11)

<221> unsure
 <222> (18)...(23)

<221> unsure
 <222> (34)...(34)

<221> unsure
 <222> (37)...(38)

<221> unsure
 <222> (40)...(42)

<221> unsure
 <222> (50)...(52)

<221> unsure
 <222> (55)...(58)

<221> unsure
 <222> (152)...(152)

<221> unsure
 <222> (155)...(155)

1011c2PCTSEQUENCE LISTING

<221> unsure

<222> (165)...(165)

<400> 107

nttttttttg ngcgcacnnn nnnngnnnncg ccenggnngn nnagcctacn nncannnnngt
 60
 tttcttctcc aggctgaaga cctgaacgtc aagttggaag gggagccttc catgcggaaa
 120
 ccaaagcagc ggccgcggcc ggagcccctc ancancccca ccaangcggg cactttcatc
 180
 gccctctctg tctactccaa catcaccctc taccaga
 217

<210> 108

<211> 346

<212> DNA

<213> mouse

<220>

<400> 108

gggcatagaa ggcattctga aaagaatact tatttgaatt gaaggaagat gaagaggcct
 60
 gcaggaaggc tcagaagaca ggagtgtttt acctctttca tgacctggat cctttgctcc
 120
 aggcgtcagg acatcgatac ctgggtgccc ggcttagccg agcagagttg gaagggctgc
 180
 tgggtaagtt cggacaggat tcgcaaagaa ttgaagattc ggtgctggtt ggggtgctccg
 240
 agcagcagga agcatggttt gctttggatc taggtctgaa gagtgcctcc tccagccgtg
 300
 gacaagtatc gctgctccag cagcttgact gctgtaaaga ggatct
 346

<210> 109

<211> 242

<212> DNA

<213> mouse

<400> 109

ccacattgtc cacaactgga aggcacgatg gttcatcctt cggcagaaca cgctcctgta
 60
 ttacaagcta gaggggtggcc ggcgagtaac cccgcccag gggaggattg tccttgatgg
 120
 ctgcaccatc acctgcccct gcctggagta tgaaaaccgg ccgctcctca ttaaactgaa
 180
 gaccggaact tccactgagt acttcctgga agcctgttct cgagaggaga gagactcctg
 240
 gg
 242

<210> 110

<211> 310

<212> DNA

<213> mouse

1011c2PCTSEQUENCE LISTING

<220>

<400> 110

cccggccggg aatccaggtg gtagctggtg gagtcgcctc cggagagtga cgcgcagact
 60
 cggtccccc gcggcccgcc ctctgccgg cctcgccgcg gtctcccttg ctccctgaga
 120
 tcgtgagcg ctgagcagcg gcccgggaga ggaggccttg ggcgacgggg cgcggagagg
 180
 gagggcgggc gggcagtggg ggcgccgcg atctctatat ggcgacggct ctgtcgggtc
 240
 tggctgtccg gctgtcgcg tcggccgnc cgcccgtcc tatggggtct tctgcaa-gg
 300
 ggctgacccg
 310

<210> 111

<211> 228

<212> DNA

<213> mouse

<400> 111

ttctttttta acatttggtg gtttttttct ttactctttt tttcttttcc ttctttttct
 60
 gccctcaacc ccccaactcc tttggtatga agtactttta acatttatat ttcattgtta
 120
 cactttaaat tttgtaagga aaactctgat atttcattcc tctgaacca ctaatgtag
 180
 aatttatattc taagaatcag tcaacatgta tactcttaat agtgaatt
 228

<210> 112

<211> 292

<212> DNA

<213> mouse

<400> 112

gtggggtccc agacttgcca accaaagggc cattcctggt atatggttct ggcttcagct
 60
 ctggtggcat ggactatggt atggttggtg gcaaggaggc tgggaccgag tctcgcttca
 120
 aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc
 180
 acaaaaacgg cgctatagtg gcccctggta agacccgagg aggttcacca tacaaccagt
 240
 ttgatataat ccaggtgac aactgggtg gccatacggg tctgctggt ga
 292

<210> 113

<211> 255

<212> DNA

<213> mouse

<220>

1011c2PCTSEQUENCE LISTING

<400> 113
ttagatgact taggacttta atgttttcca tgcagtcgat tgaaaacact gatacatgaa
60
caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccctgggttaa
120
actacaagaa cagccacgtg atcacagttt gaggggtggaa ggcaggggtg tgactgagtt
180
ttgtttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa
240
acgagagtca tgggtg
255

<210> 114
<211> 197
<212> DNA
<213> mouse

<400> 114
gaccacatg tgaacagccg cgtgtatgtc aactgctct gtgtgtgatt tcttcacgtg
60
tgcattgtgc ctcttgggtt ttccacttat tgcctcgttc gtaagaaacc aaccataagg
120
tgccaaggag gttttattcc tttttttttt aaagatgaca aatgtacaga tgtagtagta
180
gatgttaatg tacagat
197

<210> 115
<211> 205
<212> DNA
<213> mouse

<400> 115
aaaacatttc acaaaacagc aaaacaaaat tgatacaatc aaaaaaacia cactataacc
60
aacatagggtg aaaacagcca aacacataat gtacaatctg gtgttccagg acaaacatct
120
gtcatatata tggatatata atatatactt tttcactcaa tatattatga caatatatat
180
ttaaaatttt gttatagaca aaaaa
205

<210> 116
<211> 202
<212> DNA
<213> mouse

<220>

<400> 116
cctccctcat cctctacttc ctttttcctt cctgcttgat tttctcattc cagaccctta
60
tgcacacaca cacacacaca cacacacaca cagcaacaca cgcacacaca cacacacacg

1011c2PCTSEQUENCE LISTING

120
 cacacacaca ctgtccatcc atagttactt atttagtttt ccattcctag agagatctaa
 180
 tcatccccta gtcagtgcc .aa
 202

<210> 117
 <211> 240
 <212> DNA
 <213> mouse.

<400> 117
 ccgccaggag aggagataca cagccagtga tgtggaccac cggatggctg ttgctgctgc
 60
 cgcttctgct gtgtgaagga gcgcaagccc tggagtgcta cagctgcgtg cagaaggcgg
 120
 acgatggatg cgctccgcac aggatgaaga cagtcaaata tggccccggg gtggacgtct
 180
 gtaccgaggc cgtgggagcg gtagagacca tccacgggca attctctgtg gcggtgcggg
 240

<210> 118
 <211> 527
 <212> DNA
 <213> Human

<400> 118
 ccgtcagtct agaaggataa gagaaagaaa gttaagcaac tacaggaaat ggctttggga
 60
 gttccaatat cagtctatct tttattcaac gcaatgacag cactgaccga agaggcagcc
 120
 gtgactgtaa cacctccaat cacagcccag caaggtaact ggacagttaa caaaacagaa
 180
 gtcacaaca tagaaggacc catagccttg aagttctcac acctttgcct ggaagatcat
 240
 aacagttact gcatcaacgg tgcttgtgca ttccaccatg agctagagaa agccatctgc
 300
 aggtgtttta ctggttatac tggagaaagg tgtgagcact tgactttaac ttcatatgct
 360
 gtggattctt atgaaaaata cattgcaatt gggattgggt ttggattact attaagtgg
 420
 tttcttgta ttttttactg ctatataaga aagaggtgtc taaaattgaa atcgccttac
 480
 aatgtctgtt ctggagaaag acgaccactg tgaggccttt gtgaaga
 527

<210> 119
 <211> 655
 <212> DNA
 <213> Rat

<400> 119
 atggcgcgcc ccgcgcctg gtggtggctg cggccgctgg cggcgctcgc cctggcgctg
 60
 gcgctgggtcc ggggtgccctc agcccgggccc gggcagatgc cgcgccccgc agagcgcggg

1011c2PCTSEQUENCE LISTING

120
 cccccagtac ggctcttcac cgaggaggag ctggcccgc acagcggcga ggaggaggat
 180
 caacccatct acttggcagt gaagggagtg gtgttcgatg tcacctctgg gaaggagttt
 240
 tatggacgtg gagcccccta caacgccttg gccgggaagg actcgagcag aggtgtggcc
 300
 aagatgtcgc tggatcctgc agacctcact catgacattt ctggtctcac tgccaaggag
 360
 ctggaagccc tcgatgacat cttcagcaag gtgtacaaag ccaaataccc cattgttggc
 420
 tacacggccc gcaggatcct caacgaggat ggcagcccca acctggactt caagcctgaa
 480
 gaccagcccc attttgacat aaaggacgag ttctaattgtc tagctgagaa gctggttcta
 540
 gggagaggtg aggggacagg agttaaatgt cccacggaac aagcagggga agcctctgag
 600
 tgctctgcat ctgaataaaa ctgatattta actgggaaaa aaaaaaaaaa aaaaa
 655

<210> 120

<211> 176

<212> PRT

<213> Rat

<400> 120

Met	Val	Pro	Cys	Phe	Leu	Leu	Ser	Leu	Leu	Leu	Leu	Val	Arg	Pro	Ala	1	5	10	15
Pro	Val	Val	Ala	Tyr	Ser	Val	Ser	Leu	Pro	Ala	Ser	Phe	Leu	Glu	Glu	20	25	30	
Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	35	40	45	
Leu	Leu	Pro	Pro	Arg	Thr	Pro	Ala	Phe	Ser	Pro	Thr	Pro	Gly	Arg	Thr	50	55	60	
Gln	Pro	Thr	Ala	Pro	Val	Gly	Pro	Val	Pro	Pro	Thr	Asn	Leu	Leu	Asp	65	70	75	80
Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	85	90	95	
Gly	Ser	Leu	Thr	Phe	Leu	Ile	Met	Phe	Ile	Val	Cys	Ala	Ala	Leu	Ile	100	105	110	
Thr	Arg	Gln	Lys	His	Lys	Ala	Thr	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	115	120	125	
Glu	Lys	Lys	Tyr	Val	Asp	Gln	Arg	Asp	Arg	Ala	Gly	Gly	Pro	His	Ala	130	135	140	
Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Gln	Glu	Glu	Gly	145	150	155	160
Leu	Asp	Phe	Phe	Gln	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Cys	Tyr	Ser	165	170	175	

<210> 121

<211> 116

<212> PRT

<213> Rat

<400> 121

1011c2PCTSEQUENCE LISTING

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
 35 40 45
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
 50 55 60
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
 65 70 75 80
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
 85 90 95
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
 100 105 110
 Gln Lys Gln Gln
 115

<210> 122
 <211> 64
 <212> PRT
 <213> Human

<400> 122

Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu
 1 5 10 15
 Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser
 20 25 30
 Val Leu Asn His Ile Ser Ser Ser Ser Ser Val Trp His Leu Phe
 35 40 45
 Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly
 50 55 60

<210> 123
 <211> 68
 <212> PRT
 <213> Human

<400> 123

Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg
 1 5 10 15
 Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly
 20 25 30
 Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr
 35 40 45
 Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe
 50 55 60
 Ser Cys Leu Leu
 65

<210> 124
 <211> 110
 <212> PRT
 <213> mouse

<400> 124

1011c2PCTSEQUENCE LISTING

Met	Ile	Ser	Pro	Ala	Trp	Ser	Leu	Phe	Leu	Ile	Gly	Thr	Lys	Ile	Gly
1				5					10					15	
Leu	Phe	Phe	Gln	Val	Ala	Pro	Leu	Ser	Val	Val	Ala	Lys	Ser	Cys	Pro
			20					25					30		
Ser	Val	Cys	Arg	Cys	Asp	Ala	Gly	Phe	Ile	Tyr	Cys	Asn	Asp	Arg	Ser
		35					40					45			
Leu	Thr	Ser	Ile	Pro	Val	Gly	Ile	Pro	Glu	Asp	Ala	Thr	Thr	Leu	Tyr
	50					55					60				
Leu	Gln	Asn	Asn	Gln	Ile	Asn	Asn	Val	Gly	Ile	Pro	Ser	Asp	Leu	Lys
65					70					75					80
Asn	Leu	Leu	Lys	Val	Gln	Arg	Ile	Tyr	Leu	Tyr	His	Asn	Ser	Leu	Asp
				85					90					95	
Glu	Phe	Pro	Thr	Asn	Leu	Pro	Lys	Tyr	Val	Lys	Glu	Leu	His		
			100					105					110		

<210> 125

<211> 330

<212> PRT

<213> mouse

<400> 125

Met	Gly	Ser	Pro	Arg	Leu	Ala	Ala	Leu	Leu	Leu	Ser	Leu	Pro	Leu	Leu
1				5					10					15	
Leu	Ile	Gly	Leu	Ala	Val	Ser	Ala	Arg	Val	Ala	Cys	Pro	Cys	Leu	Arg
			20					25					30		
Ser	Trp	Thr	Ser	His	Cys	Leu	Leu	Ala	Tyr	Arg	Val	Asp	Lys	Arg	Phe
		35					40					45			
Ala	Gly	Leu	Gln	Trp	Gly	Trp	Phe	Pro	Leu	Leu	Val	Arg	Lys	Ser	Lys
	50				55						60				
Ser	Pro	Pro	Lys	Phe	Glu	Asp	Tyr	Trp	Arg	His	Arg	Thr	Pro	Ala	Ser
65					70					75					80
Phe	Gln	Arg	Lys	Leu	Leu	Gly	Ser	Pro	Ser	Leu	Ser	Glu	Glu	Ser	His
			85					90						95	
Arg	Ile	Ser	Ile	Pro	Ser	Ser	Ala	Ile	Ser	His	Arg	Gly	Gln	Arg	Thr
			100					105					110		
Lys	Arg	Ala	Gln	Pro	Ser	Ala	Ala	Glu	Gly	Arg	Glu	His	Leu	Pro	Glu
		115					120					125			
Ala	Gly	Ser	Gln	Lys	Cys	Gly	Gly	Pro	Glu	Phe	Ser	Phe	Asp	Leu	Leu
	130					135					140				
Pro	Glu	Val	Gln	Ala	Val	Arg	Val	Thr	Ile	Pro	Ala	Gly	Pro	Lys	Ala
145					150					155					160
Ser	Val	Arg	Leu	Cys	Tyr	Gln	Trp	Ala	Leu	Glu	Cys	Glu	Asp	Leu	Ser
			165						170					175	
Ser	Pro	Phe	Asp	Thr	Gln	Lys	Ile	Val	Ser	Gly	Gly	His	Thr	Val	Asp
			180					185					190		
Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Met	Cys	Ile	Glu	Ala	Ser	Tyr
		195					200					205			
Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser	Trp
	210					215					220				
Pro	Glu	Ala	Tyr	Gly	Ser	Asp	Phe	Trp	Gln	Ser	Ile	Arg	Phe	Thr	Asp
225					230					235					240
Tyr	Ser	Gln	His	Asn	Gln	Met	Val	Met	Ala	Leu	Thr	Leu	Arg	Cys	Pro
			245						250					255	
Leu	Lys	Leu	Glu	Ala	Ser	Leu	Cys	Trp	Arg	Gln	Asp	Pro	Leu	Thr	Pro
			260					265					270		

1011c2PCTSEQUENCE LISTING

Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
 275 280 285
 Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
 290 295 300
 Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
 305 310 315 320
 Pro Ser Trp Thr Val Ser Met Asp Thr Gln
 325 330

<210> 126

<211> 37

<212> PRT

<213> Rat

<400> 126

Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
 1 5 10 15
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
 20 25 30
 Arg Ala Asp Val Leu
 35

<210> 127

<211> 42

<212> PRT

<213> mouse

<400> 127

Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
 1 5 10 15
 Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
 20 25 30
 Ser Leu His Thr Met Ser Ala Gly Phe Pro
 35 40

<210> 128

<211> 253

<212> PRT

<213> mouse

<400> 128

Met Met Tyr Trp Ile Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe
 1 5 10 15
 Thr Asp Ile Phe Ile Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp
 20 25 30
 Gly Trp Glu Gly Pro His His His His Leu Ala Ser Gly Ser His
 35 40 45
 Lys Pro Leu Pro Leu Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe
 50 55 60
 Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala
 65 70 75 80
 Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His Glu
 85 90 95
 Lys Glu Ile Asp Ala Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu
 100 105 110

1011c2PCTSEQUENCE LISTING

Thr Met Leu Ser Phe Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala
 115 120 125
 Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu
 130 135 140
 Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val
 145 150 155 160
 Pro Thr Tyr Gln Asp Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg
 165 170 175
 Arg Pro Pro Ile Gly Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr
 180 185 190
 Glu Asp Glu Cys Trp Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val
 195 200 205
 Arg Pro Arg Glu Lys Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val
 210 215 220
 Lys Arg Lys Pro Leu Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val
 225 230 235 240
 Arg Thr Arg Lys Lys Ala Met Pro Ser Asp Met Asp Ser
 245 250

<210> 129
 <211> 40
 <212> PRT
 <213> mouse

<400> 129
 Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
 1 5 10 15
 Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
 20 25 30
 Ser Lys Val Pro Gln Phe Leu Asn
 35 40

<210> 130
 <211> 87
 <212> PRT
 <213> mouse

<400> 130
 Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
 1 5 10 15
 Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
 20 25 30
 Ser Asn Ile Arg Val Thr Val Thr Ala Val Ile Ile Asn Leu
 35 40 45
 Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp
 50 55 60
 Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met
 65 70 75 80
 Gly Leu Gly Gln Gly Gln Pro
 85

<210> 131
 <211> 70
 <212> PRT
 <213> mouse

1011c2PCTSEQUENCE LISTING

> 131
y Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
5 10 15
l Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
20 25 30
s Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
40 45
s Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
55 60
r Leu Ile Ser
70

> 132
> 63
> PRT
> mouse

> 132
u Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
5 10 15
r Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
20 25 30
s Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
40 45
u Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
55 60

> 133
> 39
> PRT
> mouse

> 133
n Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
5 10 15
l Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
20 25 30
p Leu Glu Val Thr

> 134
> 90
> PRT
> Rat

> 134
r Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
5 10 15
r Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
20 25 30
s Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
40 45
g Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
55 60

1011c2PCTSEQUENCE LISTING

<400> 131
 Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
 1 5 10 15
 Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
 20 25 30
 Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
 35 40 45
 Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
 50 55 60
 Gly Leu Ser Leu Ile Ser
 65 70

<210> 132
 <211> 63
 <212> PRT
 <213> mouse

<400> 132
 Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
 1 5 10 15
 Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
 20 25 30
 Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
 35 40 45
 Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
 50 55 60

<210> 133
 <211> 39
 <212> PRT
 <213> mouse

<400> 133
 Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
 1 5 10 15
 Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
 20 25 30
 Ser Lys Asp Leu Glu Val Thr
 35

<210> 134
 <211> 90
 <212> PRT
 <213> Rat

<400> 134
 Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
 1 5 10 15
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
 20 25 30
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
 35 40 45
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
 50 55 60

1011c2PCTSEQUENCE LISTING

Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
 65 70 75 80
 Ala Gly Glu Val Leu Gly Ile Cys His Ser
 85 90

<210> 135

<211> 193

<212> PRT

<213> Rat

<400> 135

Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
 1 5 10 15
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20 25 30
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35 40 45
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50 55 60
 Tyr His Ser Phe Val Ser Ser Val Phe Thr Leu Phe Met Ser Arg Thr
 65 70 75 80
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85 90 95
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
 100 105 110
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
 115 120 125
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
 130 135 140
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
 145 150 155 160
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
 165 170 175
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Met
 180 185 190
 Ser

<210> 136

<211> 106

<212> PRT

<213> Rat

<400> 136

Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1 5 10 15
 Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Ser
 20 25 30
 Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
 35 40 45
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala
 50 55 60
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
 65 70 75 80
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr

1011c2PCTSEQUENCE LISTING

85 90 95
 Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys
 100 105
 <210> 137
 <211> 286
 <212> PRT
 <213> Rat
 <400> 137
 Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
 1 5 10 15
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
 20 25 30
 Arg Glu Glu Leu Val Ile Thr Pro Ser Gly Asp Val Ala Ala
 35 40 45
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
 50 55 60
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
 65 70 75 80
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
 85 90 95
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
 100 105 110
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
 115 120 125
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
 130 135 140
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
 145 150 155 160
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
 165 170 175
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
 180 185 190
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
 195 200 205
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
 210 215 220
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
 225 230 235 240
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
 245 250 255
 Lys Lys Glu Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp
 260 265 270
 Ile Thr Gly Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser
 275 280 285

<210> 138
 <211> 198
 <212> PRT
 <213> Rat

<400> 138
 Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
 1 5 10 15

1011c2PCTSEQUENCE LISTING

Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
 20 25 30
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
 35 40 45
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
 50 55 60
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
 65 70 75 80
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
 85 90 95
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
 100 105 110
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
 115 120 125
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
 130 135 140
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
 145 150 155 160
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
 165 170 175
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
 180 185 190
 Ser Gly Lys Phe Val Cys
 195

<210> 139

<211> 233

<212> PRT

<213> Rat

<400> 139

Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1 5 10 15
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20 25 30
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35 40 45
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50 55 60
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65 70 75 80
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85 90 95
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100 105 110
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115 120 125
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130 135 140
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145 150 155 160
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
 165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190

1011c2PCTSEQUENCE LISTING

Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe Leu Gln Pro Gly
 225 230

<210> 140
 <211> 38
 <212> PRT
 <213> Human

<400> 140
 Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg
 1 5 10 15
 Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu
 20 25 30
 Ile Asp Thr Val Asp Leu
 35

<210> 141
 <211> 322
 <212> PRT
 <213> mouse

<400> 141
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
 20 25 30
 Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
 85 90 95
 Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
 100 105 110
 Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
 115 120 125
 Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

1011c2PCTSEQUENCE LISTING

225					230					235					240
Leu	Thr	Ala	Gly	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser
				245					250					255	
Ser	Gly	Pro	Glu	Pro	Arg	Ser	Ser	Pro	Ala	Thr	Thr	Leu	Ser	Gly	Leu
			260					265					270		
Val	Leu	Leu	Ala	Gly	Tyr	Ile	Ala	Phe	Asp	Ser	Phe	Thr	Ser	Asn	Trp
		275					280					285			
Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Lys	Met	Ser	Ser	Val	Gln	Met	Met	Phe
	290					295					300				
Gly	Val	Asn	Leu	Phe	Ser	Cys	Leu	Phe	Thr	Val	Gly	Ser	Leu	Leu	Glu
305					310					315					320
Gln	Gly														

<210> 142
 <211> 312
 <212> PRT
 <213> mouse

<400> 142

Met	Leu	Cys	Leu	Cys	Leu	Tyr	Val	Pro	Ile	Ala	Gly	Ala	Ala	Gln	Thr
1				5					10					15	
Glu	Phe	Gln	Tyr	Phe	Glu	Ser	Lys	Gly	Leu	Pro	Ala	Glu	Leu	Lys	Ser
			20					25					30		
Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe	Ser	Thr	Tyr
		35					40					45			
Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp	Lys	Asp	Leu	Asp
	50					55					60				
Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr	Leu	Gln	Asp	His	Glu
65					70					75				80	
Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ser	Leu	Asp	Lys	Lys	Asn	Asp	Gly
			85						90					95	
Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	Ser	Leu	Arg	Asp	Leu	Gly	Val
			100					105					110		
Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys
		115					120					125			
Asn	Gly	Thr	Met	Thr	Ile	Asp	Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu
	130					135					140				
Leu	His	Pro	Val	Glu	Asn	Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His
145					150					155				160	
Ser	Thr	Ile	Phe	Asp	Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe
				165					170					175	
Thr	Val	Glu	Glu	Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala
			180					185					190		
Gly	Gly	Gly	Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp
		195					200					205			
Arg	Leu	Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met
	210					215						220			
Cys	Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Lys
225					230					235					240
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	Glu
				245					250					255	
Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Met	Lys	Arg	Leu	Val	Gly
			260					265					270		
Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	Ala	Gly	Ser

1011c2PCTSEQUENCE LISTING

	275		280		285
Leu	Ala Gly	Ala Ile	Ala Gln	Ser Ser Ile Tyr	Pro Met Glu Val Leu
	290		295		300
Lys	Thr Arg	Met Ala	Leu Arg	Lys	
305			310		

<210> 143

<211> 163

<212> PRT

<213> Rat

<400> 143

Met	Pro	Leu	Val	Thr	Thr	Leu	Phe	Tyr	Ala	Cys	Phe	Tyr	His	Tyr	Thr
1			5					10					15		
Glu	Ser	Glu	Gly	Thr	Phe	Ser	Ser	Pro	Val	Asn	Leu	Lys	Lys	Thr	Phe
		20					25					30			
Lys	Ile	Pro	Asp	Arg	Gln	Tyr	Val	Leu	Thr	Ala	Leu	Ala	Ala	Arg	Ala
	35					40					45				
Lys	Leu	Arg	Ala	Trp	Asn	Asp	Val	Asp	Ala	Leu	Phe	Thr	Thr	Lys	Asn
	50				55						60				
Trp	Leu	Gly	Tyr	Thr	Lys	Lys	Arg	Ala	Pro	Ile	Gly	Phe	His	Arg	Val
65				70					75						80
Val	Glu	Ile	Leu	His	Lys	Asn	Ser	Ala	Pro	Val	Gln	Ile	Leu	Gln	Glu
			85					90					95		
Tyr	Val	Asn	Leu	Val	Glu	Asp	Val	Asp	Thr	Lys	Leu	Asn	Leu	Ala	Thr
		100					105					110			
Lys	Phe	Lys	Cys	His	Asp	Val	Val	Ile	Asp	Thr	Cys	Arg	Asp	Leu	Lys
	115					120					125				
Asp	Arg	Gln	Gln	Leu	Leu	Ala	Tyr	Arg	Ser	Lys	Val	Asp	Lys	Gly	Ser
	130				135					140					
Ala	Glu	Glu	Glu	Lys	Ile	Asp	Val	Ile	Leu	Ser	Ser	Ser	Gln	Ile	Arg
145				150					155						160
Trp	Lys	Asn													

<210> 144

<211> 330

<212> PRT

<213> Rat

<400> 144

Met	Ala	Gly	Trp	Ala	Gly	Ala	Glu	Leu	Ser	Val	Leu	Asn	Pro	Leu	Arg
1			5					10					15		
Ala	Leu	Trp	Leu	Leu	Ala	Ala	Ala	Phe	Leu	Leu	Ala	Leu	Leu	Leu	
		20					25					30			
Gln	Leu	Ala	Pro	Ala	Arg	Leu	Leu	Pro	Ser	Cys	Ala	Leu	Phe	Gln	Asp
	35					40					45				
Leu	Ile	Arg	Tyr	Gly	Lys	Thr	Lys	Gln	Ser	Gly	Ser	Arg	Arg	Pro	Ala
	50				55					60					
Val	Cys	Arg	Ala	Phe	Asp	Val	Pro	Lys	Arg	Tyr	Phe	Ser	His	Phe	Tyr
65				70					75						80
Val	Val	Ser	Val	Leu	Trp	Asn	Gly	Ser	Leu	Leu	Trp	Phe	Leu	Ser	Gln
			85				90					95			
Ser	Leu	Phe	Leu	Gly	Ala	Pro	Phe	Pro	Ser	Trp	Leu	Trp	Ala	Leu	Leu
		100					105						110		

1011c2PCTSEQUENCE LISTING

Arg	Thr	Leu	Gly	Val	Thr	Gln	Phe	Gln	Ala	Leu	Gly	Met	Glu	Ser	Lys		
		115					120					125					
Ala	Ser	Arg	Ile	Gln	Ala	Gly	Glu	Leu	Ala	Leu	Ser	Thr	Phe	Leu	Val		
		130				135					140						
Leu	Val	Phe	Leu	Trp	Val	His	Ser	Leu	Arg	Arg	Leu	Phe	Glu	Cys	Phe		
145					150					155					160		
Tyr	Val	Ser	Val	Phe	Ser	Asn	Thr	Ala	Ile	His	Val	Val	Gln	Tyr	Cys		
				165					170					175			
Phe	Gly	Leu	Val	Tyr	Tyr	Val	Leu	Val	Gly	Leu	Thr	Val	Leu	Ser	Gln		
			180					185				190					
Val	Pro	Met	Asn	Asp	Lys	Asn	Val	Tyr	Ala	Leu	Gly	Lys	Asn	Leu	Leu		
		195				200						205					
Leu	Gln	Ala	Arg	Trp	Phe	His	Ile	Leu	Gly	Met	Met	Met	Phe	Phe	Trp		
		210				215					220						
Ser	Ser	Ala	His	Gln	Tyr	Lys	Cys	His	Val	Ile	Leu	Ser	Asn	Leu	Arg		
225					230					235					240		
Arg	Asn	Lys	Lys	Gly	Val	Val	Ile	His	Cys	Gln	His	Arg	Ile	Pro	Phe		
				245					250					255			
Gly	Asp	Trp	Phe	Glu	Tyr	Val	Ser	Ser	Ala	Asn	Tyr	Leu	Ala	Glu	Leu		
			260					265					270				
Met	Ile	Tyr	Ile	Ser	Met	Ala	Val	Thr	Phe	Gly	Leu	His	Asn	Val	Thr		
		275					280					285					
Trp	Trp	Leu	Val	Val	Thr	Tyr	Val	Phe	Phe	Ser	Gln	Ala	Leu	Ser	Ala		
		290				295					300						
Phe	Phe	Asn	His	Arg	Phe	Tyr	Lys	Ser	Thr	Phe	Val	Ser	Tyr	Pro	Lys		
305					310					315					320		
His	Arg	Lys	Ala	Phe	Leu	Pro	Phe	Leu	Phe								
				325					330								

<210> 145

<211> 301

<212> PRT

<213> Rat

<400> 145

Met	Leu	Val	Ala	Phe	Leu	Gly	Ala	Ser	Ala	Val	Thr	Ala	Ser	Thr	Gly		
1				5					10					15			
Leu	Leu	Trp	Lys	Lys	Ala	His	Ala	Glu	Ser	Pro	Pro	Ser	Val	Asn	Ser		
			20					25					30				
Lys	Lys	Thr	Asp	Ala	Gly	Asp	Lys	Gly	Lys	Ser	Lys	Asp	Thr	Arg	Glu		
		35				40						45					
Val	Ser	Ser	His	Glu	Gly	Ser	Ala	Ala	Asp	Thr	Ala	Ala	Glu	Pro	Tyr		
		50				55					60						
Pro	Glu	Glu	Lys	Lys	Lys	Lys	Arg	Ser	Gly	Phe	Arg	Asp	Arg	Lys	Val		
65					70					75					80		
Met	Glu	Tyr	Glu	Asn	Arg	Ile	Arg	Ala	Tyr	Ser	Thr	Pro	Asp	Lys	Ile		
			85						90					95			
Phe	Arg	Tyr	Phe	Ala	Thr	Leu	Lys	Val	Ile	Asn	Glu	Pro	Gly	Glu	Thr		
			100					105					110				
Glu	Val	Phe	Met	Thr	Pro	Gln	Asp	Phe	Val	Arg	Ser	Ile	Thr	Pro	Asn		
		115					120					125					
Glu	Lys	Gln	Pro	Glu	His	Leu	Gly	Leu	Asp	Gln	Tyr	Ile	Ile	Lys	Arg		
		130				135					140						
Phe	Asp	Gly	Lys	Lys	Ile	Ala	Gln	Glu	Arg	Glu	Lys	Phe	Ala	Asp	Glu		
145					150					155					160		

1011c2PCTSEQUENCE LISTING

Gly	Ser	Ile	Phe	Tyr	Thr	Leu	Gly	Glu	Cys	Gly	Leu	Ile	Ser	Phe	Ser
				165					170					175	
Asp	Tyr	Ile	Phe	Leu	Thr	Thr	Val	Leu	Ser	Thr	Pro	Gln	Arg	Asn	Phe
			180					185					190		
Glu	Ile	Ala	Phe	Lys	Met	Phe	Asp	Leu	Asn	Gly	Asp	Gly	Glu	Val	Asp
		195					200					205			
Met	Glu	Glu	Phe	Glu	Gln	Val	Gln	Ser	Ile	Ile	Arg	Ser	Gln	Thr	Ser
	210					215					220				
Met	Gly	Met	Arg	His	Arg	Asp	Arg	Pro	Thr	Thr	Gly	Asn	Thr	Leu	Lys
225					230						235				240
Ser	Gly	Leu	Cys	Ser	Ala	Leu	Thr	Thr	Tyr	Phe	Phe	Gly	Ala	Asp	Leu
			245						250					255	
Lys	Gly	Lys	Leu	Thr	Ile	Lys	Asn	Phe	Leu	Glu	Phe	Gln	Arg	Lys	Leu
			260					265					270		
Gln	Arg	Cys	Leu	Leu	Gly	Leu	Pro	Val	Trp	Glu	Gly	Ser	Pro	His	Leu
		275					280					285			
Pro	Thr	Gly	His	Trp	Leu	Arg	Glu	Leu	Trp	Ser	Leu	Leu			
	290					295					300				

<210> 146

<211> 61

<212> PRT

<213> Rat

<400> 146

Met	Glu	Asn	Ile	Tyr	Tyr	Thr	Asn	Leu	Ile	Thr	Ile	Leu	Gly	Asn	Lys
1				5					10					15	
His	Ala	Asn	Gln	Met	Glu	Leu	Asn	Leu	Gln	Ala	Leu	Ile	Leu	Ser	Pro
			20					25					30		
Trp	Phe	Ala	Val	Cys	Ala	Pro	Pro	Gly	Phe	Ala	Arg	Asp	Gln	Ala	Val
		35					40					45			
Arg	Gly	Leu	Ala	Leu	Ala	Gly	Arg	Arg	Ile	Thr	Val	Val			
	50					55					60				

<210> 147

<211> 105

<212> PRT

<213> Rat

<400> 147

Met	Leu	Arg	Arg	Gln	Leu	Val	Trp	Trp	His	Leu	Leu	Ala	Leu	Leu	Phe
1				5					10					15	
Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Ser	Pro	Gln	Ala
			20					25					30		
Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly	Asp	Tyr	Gly
		35					40					45			
Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile	
	50					55					60				
Pro	Gly	Asn	His	Gly	Asn	Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu	
65					70				75					80	
Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly
				85					90					95	
Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly							
			100					105							

1011c2PCTSEQUENCE LISTING

<210> 148
 <211> 210
 <212> PRT
 <213> Rat

<400> 148
 Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val
 1 5 10 15
 Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
 20 25 30
 Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
 35 40 45
 Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
 50 55 60
 Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His
 65 70 75 80
 Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
 85 90 95
 Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
 100 105 110
 His Leu Gln Thr Pro Leu Gln Ala Trp Arg Thr Arg Ala Lys Leu Pro
 115 120 125
 Pro Gly Gly Thr Glu Ala Val Pro Gly Arg Pro Gly Ala Gln Gln Asp
 130 135 140
 Ala Cys His Leu Leu Tyr Trp Thr Tyr Asn Gly Val Ser Ser Ile Pro
 145 150 155 160
 Cys His Arg Gly Gly Leu Ser His Val Pro Ser Glu Val Pro Ala Glu
 165 170 175
 Lys Ser Pro Val Leu Ile Leu His Ala Ala Pro Pro Phe Lys Thr Pro
 180 185 190
 Val Asn Pro Trp Ala Arg Thr Val Val Gly Phe Phe Pro Ser Ser Pro
 195 200 205
 Ser Leu
 210

<210> 149
 <211> 301
 <212> PRT
 <213> Rat

<400> 149
 Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1 5 10 15
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
 20 25 30
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
 35 40 45
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
 50 55 60
 Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
 65 70 75 80
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
 85 90 95
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
 100 105 110

1011c2PCTSEQUENCE LISTING

Glu	Val	Phe	Met	Thr	Pro	Gln	Asp	Phe	Val	Arg	Ser	Ile	Thr	Pro	Asn
		115					120					125			
Glu	Lys	Gln	Pro	Glu	His	Leu	Gly	Leu	Asp	Gln	Tyr	Ile	Ile	Lys	Arg
		130					135				140				
Phe	Asp	Gly	Lys	Lys	Ile	Ala	Gln	Glu	Arg	Glu	Lys	Phe	Ala	Asp	Glu
145					150					155					160
Gly	Ser	Ile	Phe	Tyr	Thr	Leu	Gly	Glu	Cys	Gly	Leu	Ile	Ser	Phe	Ser
				165					170					175	
Asp	Tyr	Ile	Phe	Leu	Thr	Thr	Val	Leu	Ser	Thr	Pro	Gln	Arg	Asn	Phe
			180					185					190		
Glu	Ile	Ala	Phe	Lys	Met	Phe	Asp	Leu	Asn	Gly	Asp	Gly	Glu	Val	Asp
		195					200					205			
Met	Glu	Glu	Phe	Glu	Gln	Val	Gln	Ser	Ile	Ile	Arg	Ser	Gln	Thr	Ser
		210				215					220				
Met	Gly	Met	Arg	His	Arg	Asp	Arg	Pro	Thr	Thr	Gly	Asn	Thr	Leu	Lys
225					230					235					240
Ser	Gly	Leu	Cys	Ser	Ala	Leu	Thr	Thr	Tyr	Phe	Phe	Gly	Ala	Asp	Leu
				245					250					255	
Lys	Gly	Lys	Leu	Thr	Ile	Lys	Asn	Phe	Leu	Glu	Phe	Gln	Arg	Lys	Leu
			260					265					270		
Gln	Arg	Cys	Leu	Leu	Gly	Leu	Pro	Val	Trp	Glu	Gly	Ser	Pro	His	Leu
		275					280					285			
Pro	Thr	Gly	His	Trp	Leu	Arg	Glu	Leu	Trp	Ser	Leu	Leu			
		290				295					300				

<210> 150
 <211> 80
 <212> PRT
 <213> Human

<400> 150
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys
 35 40 45
 Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala
 50 55 60
 Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys
 65 70 75 80

<210> 151
 <211> 27
 <212> PRT
 <213> mouse

<400> 151
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1 5 10 15
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
 20 25

<210> 152
 <211> 86

1011c2PCTSEQUENCE LISTING

<212> PRT

<213> mouse

<400> 152

Met	Leu	Gln	Gly	Pro	Ala	Pro	Ser	Cys	Phe	Trp	Val	Phe	Ser	Gly	Ile
1				5					10					15	
Cys	Val	Phe	Trp	Asp	Phe	Ile	Phe	Ile	Ile	Phe	Phe	Asn	Val	Leu	Ser
			20					25					30		
Leu	Gly	Asn	Arg	Glu	Ile	Ser	Ala	Lys	Asp	Phe	Ala	Asp	Gln	Pro	Ala
		35					40					45			
Gly	Ala	Gln	Gly	Met	Trp	Gly	Ile	Trp	Gly	His	Thr	Ile	Thr	Cys	Gly
	50					55					60				
Leu	Ala	Pro	Gly	Ala	Lys	Pro	Cys	Ser	Leu	Lys	Arg	Glu	Gly	Pro	Asp
65					70					75					80
Leu	Leu	Ser	Phe	Pro	Pro										
				85											

<210> 153

<211> 72

<212> PRT

<213> mouse

<400> 153

Met	Ser	Ala	Ile	Phe	Asn	Phe	Gln	Ser	Leu	Leu	Thr	Val	Ile	Leu	Leu
1				5					10					15	
Leu	Ile	Cys	Thr	Cys	Ala	Tyr	Ile	Arg	Ser	Leu	Ala	Pro	Ser	Ile	Leu
			20					25					30		
Asp	Arg	Asn	Lys	Thr	Gly	Leu	Leu	Gly	Ile	Phe	Trp	Lys	Cys	Ala	Arg
		35					40					45			
Ile	Gly	Glu	Arg	Lys	Ser	Pro	Tyr	Val	Ala	Ile	Cys	Cys	Ile	Val	Met
	50					55					60				
Ala	Phe	Ser	Ile	Leu	Phe	Ile	Gln								
65					70										

<210> 154

<211> 169

<212> PRT

<213> mouse

<400> 154

Met	Ser	Gly	Leu	Arg	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Leu	Val	Ala	Gly
1				5					10					15	
Ser	Arg	Leu	Pro	Arg	Val	Ile	Ser	Gln	Gln	Ser	Val	Cys	Arg	Ala	Arg
			20					25					30		
Pro	Ile	Trp	Trp	Gly	Thr	Gln	Arg	Arg	Gly	Ser	Glu	Thr	Met	Ala	Gly
		35					40					45			
Ala	Ala	Val	Lys	Tyr	Leu	Ser	Gln	Glu	Glu	Ala	Gln	Ala	Val	Asp	Gln
	50					55					60				
Glu	Leu	Phe	Asn	Glu	Tyr	Gln	Phe	Ser	Val	Asp	Gln	Leu	Met	Glu	Leu
65				70						75					80
Ala	Gly	Leu	Ser	Cys	Ala	Thr	Ala	Ile	Ala	Lys	Ala	Tyr	Pro	Pro	Thr
			85						90				95		
Ser	Met	Ser	Lys	Ser	Pro	Pro	Thr	Val	Leu	Val	Ile	Cys	Gly	Pro	Gly
			100					105					110		
Asn	Asn	Gly	Gly	Asp	Gly	Leu	Val	Cys	Ala	Arg	His	Leu	Lys	Leu	Phe

1011c2PCTSEQUENCE LISTING

		115						120					125				
Gly	Tyr	Gln	Pro	Thr	Ile	Tyr	Tyr	Pro	Lys	Arg	Pro	Asn	Lys	Pro	Leu		
	130						135					140					
Phe	Thr	Gly	Leu	Val	Thr	Gln	Cys	Gln	Lys	Met	Asp	Ile	Pro	Phe	Leu		
145					150					155					160		
Gly	Glu	Met	Pro	Pro	Glu	Asp	Gly	Met									
				165													

<210> 155
 <211> 61
 <212> PRT
 <213> mouse:

Met	Glu	Lys	Gln	Met	Asp	Ala	Ser	Val	Ser	Val	Ile	Phe	Gly	Ser	Ile		
1				5					10					15			
Val	Ile	Ser	Ala	Phe	Leu	Tyr	Leu	Ser	Leu	Ala	Gly	Pro	Trp	Ala	Val		
			20					25					30				
Thr	Val	Thr	Gln	Met	Arg	Thr	Ile	Ile	Thr	Met	Asp	Gln	Leu	Arg			
		35					40				45						
Asp	Ala	Leu	Ile	Leu	Asp	Gln	Leu	Lys	Val	Ala	Val	Ser					
50						55					60						

<210> 156
 <211> 131
 <212> PRT
 <213> mouse

Met	Ala	Pro	Ser	Leu	Trp	Lys	Gly	Leu	Val	Gly	Val	Gly	Leu	Phe	Ala		
1				5					10					15			
Leu	Ala	His	Ala	Ala	Phe	Ser	Ala	Ala	Gln	His	Arg	Ser	Tyr	Met	Arg		
			20					25					30				
Leu	Thr	Glu	Lys	Glu	Asp	Glu	Ser	Leu	Pro	Ile	Asp	Ile	Val	Leu	Gln		
		35					40					45					
Thr	Leu	Leu	Ala	Phe	Ala	Val	Thr	Cys	Tyr	Gly	Ile	Val	His	Ile	Ala		
50						55					60						
Gly	Glu	Phe	Lys	Asp	Met	Asp	Ala	Thr	Ser	Glu	Leu	Lys	Asn	Lys	Thr		
65					70					75				80			
Phe	Asp	Thr	Leu	Arg	Asn	His	Pro	Ser	Phe	Tyr	Val	Phe	Asn	His	Arg		
				85					90					95			
Gly	Arg	Val	Leu	Phe	Arg	Pro	Ser	Asp	Ala	Thr	Asn	Ser	Ser	Asn	Leu		
			100					105					110				
Asp	Ala	Leu	Ser	Ser	Asn	Thr	Ser	Leu	Lys	Leu	Arg	Lys	Phe	Asp	Ser		
		115					120					125					
Leu	Arg	Arg															
130																	

<210> 157
 <211> 133
 <212> PRT
 <213> mouse

Met	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Cys		

1011c2PCTSEQUENCE LISTING

1	5	10	15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro			
	20	25	30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr			
	35	40	45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val			
	50	55	60
Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala			
65	70	75	80
Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly			
	85	90	95
Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro			
	100	105	110
Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu			
	115	120	125
Ser Phe Ser Gln Ala			
130			

<210> 158
 <211> 78
 <212> PRT
 <213> mouse

<400> 158
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
1
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
20
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
35
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
50
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65
70
75

<210> 159
 <211> 206
 <212> PRT
 <213> mouse

<400> 159
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
1
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
20
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Asn Ser
35
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
50
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
65
70
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
85
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
100
105
110

1011c2PCTSEQUENCE LISTING

Trp	Ile	Gly	Gly	Gly	Tyr	Gly	Thr	Lys	Tyr	Trp	Ser	Arg	Arg	Ser	Ser
		115					120					125			
Gln	Glu	Trp	Arg	Cys	Val	Asn	Asp	Lys	Thr	Arg	Thr	Gln	Arg	Ile	Gln
		130				135					140				
Leu	Gln	Cys	Gln	Asp	Gly	Ser	Thr	Arg	Thr	Tyr	Lys	Ile	Thr	Val	Val
145					150					155					160
Thr	Ala	Cys	Lys	Cys	Lys	Arg	Tyr	Thr	Arg	Gln	His	Asn	Glu	Ser	Ser
				165					170					175	
His	Asn	Phe	Glu	Ser	Val	Ser	Pro	Ala	Lys	Pro	Ala	Gln	His	His	Arg
			180					185					190		
Glu	Arg	Lys	Arg	Ala	Ser	Lys	Ser	Ser	Lys	His	Ser	Leu	Ser		
		195					200					205			

<210> 160
 <211> 169
 <212> PRT
 <213> mouse

<400> 160

Met	Ser	Gly	Leu	Arg	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Leu	Val	Ala	Gly
1			5					10					15		
Ser	Arg	Leu	Pro	Arg	Val	Ile	Ser	Gln	Gln	Ser	Val	Cys	Arg	Ala	Arg
			20					25				30			
Pro	Ile	Trp	Trp	Gly	Thr	Gln	Arg	Arg	Gly	Ser	Glu	Thr	Met	Ala	Gly
		35				40					45				
Ala	Ala	Val	Lys	Tyr	Leu	Ser	Gln	Glu	Glu	Ala	Gln	Ala	Val	Asp	Gln
	50					55				60					
Glu	Leu	Phe	Asn	Glu	Tyr	Gln	Phe	Ser	Val	Asp	Gln	Leu	Met	Glu	Leu
65				70				75						80	
Ala	Gly	Leu	Ser	Cys	Ala	Thr	Ala	Ile	Ala	Lys	Ala	Tyr	Pro	Pro	Thr
			85					90					95		
Ser	Met	Ser	Lys	Ser	Pro	Pro	Thr	Val	Leu	Val	Ile	Cys	Gly	Pro	Gly
			100					105					110		
Asn	Asn	Gly	Gly	Asp	Gly	Leu	Val	Cys	Ala	Arg	His	Leu	Lys	Leu	Phe
		115				120						125			
Gly	Tyr	Gln	Pro	Thr	Ile	Tyr	Tyr	Pro	Lys	Arg	Pro	Asn	Lys	Pro	Leu
	130					135					140				
Phe	Thr	Gly	Leu	Val	Thr	Gln	Cys	Gln	Lys	Met	Asp	Ile	Pro	Phe	Leu
145					150					155					160
Gly	Glu	Met	Pro	Pro	Glu	Asp	Gly	Met							
				165											

<210> 161
 <211> 114
 <212> PRT
 <213> mouse

<400> 161

Met	Ser	Val	Thr	Ile	Gly	Arg	Leu	Ala	Leu	Phe	Leu	Ile	Gly	Ile	Leu
1				5					10				15		
Leu	Cys	Pro	Val	Ala	Pro	Ser	Leu	Thr	Arg	Ser	Trp	Pro	Gly	Pro	Asp
			20					25					30		
Thr	Cys	Ser	Leu	Phe	Leu	Gln	His	Ser	Leu	Ser	Leu	Ser	Leu	Arg	Leu
		35				40					45				
Gly	Gln	Ser	Leu	Glu	Gly	Gly	Leu	Ser	Val	Cys	Phe	His	Val	Cys	Ile

1011c2PCTSEQUENCE LISTING

50
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
 65 70 75 80
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
 85 90 95
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
 100 105 110
 Ser Leu

<210> 162
 <211> 46
 <212> PRT
 <213> mouse

<400> 162
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
 1 5 10 15
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
 20 25 30
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
 35 40 45

<210> 163
 <211> 122
 <212> PRT
 <213> mouse

<400> 163
 Met Phe Thr Phe Val Val Leu Val Ile Thr Ile Val Ile Cys Leu Cys
 1 5 10 15
 His Val Cys Phe Gly His Phe Lys Tyr Leu Ser Ala His Asn Tyr Lys
 20 25 30
 Ile Glu His Thr Glu Thr Asp Ala Val Ser Ser Arg Ser Asn Gly Arg
 35 40 45
 Pro Pro Thr Ala Gly Ala Val Pro Lys Ser Ala Lys Tyr Ile Ala Gln
 50 55 60
 Val Leu Gln Asp Ser Glu Gly Asp Gly Asp Gly Asp Gly Ala Pro Gly
 65 70 75 80
 Ser Ser Gly Asp Glu Pro Pro Ser Ser Ser Ser Gln Asp Glu Glu Leu
 85 90 95
 Leu Met Pro Pro Asp Gly Leu Thr Asp Thr Asp Phe Gln Ser Cys Glu
 100 105 110
 Asp Ser Leu Ile Glu Asn Glu Ile His Gln
 115 120

<210> 164
 <211> 60
 <212> PRT
 <213> Rat

<400> 164
 Met Ser Phe Val Lys Ile Glu Ala Thr Pro Thr Gln Thr Lys Trp Pro
 1 5 10 15
 Phe Ser Val Val Pro Gln Ser Leu Leu Val Thr Val Tyr Ile Cys Tyr

1011c2PCTSEQUENCE LISTING

			20					25					30				
Ile	Phe	Leu	Val	Ile	Phe	Phe	Phe	Phe	Phe	Glu	Ala	Cys	Gln	Glu	Val		
		35					40					45					
Leu	Cys	Ser	Phe	Phe	Asp	Phe	Ser	Arg	Arg	Arg	Gly						
	50					55					60						

<210> 165
 <211> 57
 <212> PRT
 <213> mouse

Met	Gly	Ser	Pro	Ile	Ser	Gly	Val	Cys	Pro	Val	Leu	Pro	Gly	Gly	Leu		
1				5					10					15			
Phe	Val	Ala	Leu	Gly	Trp	Ile	Phe	Leu	Leu	Phe	His	Arg	Asp	Ala	Phe		
		20						25					30				
Ser	Leu	His	Thr	Met	Ser	Ala	Gly	Phe	Pro	Lys	Ser	Pro	Ala	Asn	Pro		
		35					40					45					
His	His	Pro	Pro	Leu	Arg	Leu	Ser	Pro									
	50					55											

<210> 166
 <211> 75
 <212> PRT
 <213> mouse

Lys	Thr	Arg	Arg	Thr	Leu	Thr	Gly	Gln	Leu	Gly	Leu	Phe	Ser	Val	Asp		
1				5					10					15			
Phe	Met	Val	Cys	Ile	Phe	Leu	Phe	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Pro		
		20						25					30				
Phe	Pro	Leu	Phe	Leu	Val	Arg	Lys	His	Ile	Leu	Leu	Ser	His	Cys	Lys		
		35					40					45					
Gln	Trp	Glu	Gly	Ser	Thr	Met	Thr	His	Thr	His	Thr	His	Thr	His	Ile		
	50					55						60					
His	Ile	His	Thr	Pro	Pro	Arg	Gln	Cys	Gln	Ser							
65					70					75							

<210> 167
 <211> 52
 <212> PRT
 <213> mouse

Val	Arg	Ser	Leu	Glu	Gln	Leu	Gly	Leu	Phe	Ser	Val	Asp	Phe	Met	Val		
1				5					10					15			
Cys	Ile	Phe	Leu	Phe	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Pro	Phe	Pro	Leu		
		20						25					30				
Phe	Leu	Val	Arg	Lys	His	Ile	Leu	Leu	Ser	His	Cys	Lys	Gln	Trp	Glu		
		35					40					45					
Gly	Ser	Thr	Met														
	50																

<210> 168
 <211> 119

1011c2PCTSEQUENCE LISTING

<212> PRT

<213> Rat

<400> 168

Met	Leu	Gly	Ala	Thr	Ser	Leu	Ser	Trp	Pro	Trp	Val	Leu	Trp	Ala	Val
1				5					10					15	
Ala	Gln	Arg	Asp	Ser	Val	Asp	Ala	Ile	Gly	Met	Phe	Leu	Gly	Gly	Leu
			20					25					30		
Val	Ala	Thr	Ile	Phe	Leu	Asp	Ile	Ile	Tyr	Ile	Ser	Ile	Phe	Tyr	Ser
		35					40					45			
Ser	Val	Ala	Val	Gly	Asp	Thr	Gly	Arg	Phe	Ser	Ala	Gly	Met	Ala	Ile
	50					55					60				
Phe	Ser	Leu	Leu	Leu	Gln	Ala	Leu	Leu	Leu	Leu	Pro	Arg	Leu	Pro	His
65					70					75					80
Ala	Pro	Gly	Ser	Glu	Gly	Val	Ser	Ser	Arg	Ser	Ala	Arg	Ile	Ser	Ser
				85					90					95	
Asp	Leu	Leu	Arg	Asn	Ile	Val	Pro	Thr	Arg	Gln	Leu	Thr	Arg	Gln	Thr
			100					105					110		
His	Leu	Gln	Thr	Pro	Leu	Gln									
			115												

<210> 169

<211> 104

<212> PRT

<213> Rat

<220>

<400> 169

Leu	Val	Pro	Lys	Ser	Ala	Arg	Ala	Ser	Leu	Leu	Cys	Cys	Gly	Pro	Lys
1				5					10					15	
Leu	Ala	Ala	Cys	Gly	Ile	Val	Leu	Ser	Ala	Trp	Gly	Val	Ile	Met	Leu
			20					25					30		
Ile	Met	Leu	Gly	Ile	Phe	Phe	Asn	Val	His	Ser	Ala	Val	Xaa	Ile	Xaa
		35					40					45			
Asp	Val	Pro	Phe	Thr	Glu	Lys	Asp	Phe	Glu	Asn	Gly	Pro	Gln	Asn	Ile
	50					55					60				
Tyr	Asn	Leu	Tyr	Glu	Gln	Val	Ser	Tyr	Asn	Cys	Phe	Ile	Ala	Ala	Gly
65					70					75					80
Leu	Tyr	Leu	Leu	Xaa	Gly	Gly	Phe	Ser	Phe	Cys	Gln	Val	Arg	Leu	Asn
				85					90					95	
Lys	Arg	Lys	Glu	Tyr	Met	Val	Arg								
			100												

<210> 170

<211> 123

<212> PRT

<213> Rat

<220>

<221> UNSURE

<222> (27)...(27)

<221> UNSURE

1011c2PCTSEQUENCE LISTING

<222> (104)...(104)

<221> UNSURE

<222> (118)...(118)

<400> 170

Met	Arg	Pro	Gly	Ala	Asp	Trp	Ala	Ala	Val	Cys	Ala	Leu	Trp	Pro	Ser
1				5					10					15	
Trp	Arg	Pro	Ser	Cys	Ser	Leu	Pro	Ser	Ser	Xaa	Arg	Ile	Gln	Pro	Asp
			20					25					30		
Glu	Leu	Trp	Leu	Tyr	Arg	Asn	Pro	Tyr	Val	Lys	Ala	Glu	Tyr	Phe	Pro
		35					40					45			
Thr	Gly	Pro	Met	Phe	Val	Ile	Ala	Phe	Leu	Thr	Pro	Leu	Ser	Leu	Ile
	50					55					60				
Phe	Phe	Ala	Lys	Phe	Leu	Arg	Lys	Ala	Asp	Ala	Asp	Arg	Gln	Arg	Ala
65					70					75					80
Ser	Leu	Pro	Arg	Cys	Gln	Pro	Cys	Pro	Ser	Ala	Lys	Trp	Cys	Leu	Tyr
				85					90					95	
Gln	His	His	Lys	Thr	Asp	Ser	Xaa	Gln	Gly	His	Ala	Gln	Ile	Ala	Ser
			100					105					110		
Thr	Glu	Cys	Ser	Pro	Xaa	Gly	Ile	Ala	His	Ser					
		115					120								

<210> 171

<211> 75

<212> PRT

<213> Rat

<400> 171

Ser	Ala	Gly	Val	Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile
1				5					10					15	
Ala	Phe	Gly	Pro	Ala	Leu	Ser	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Thr	Asp
			20					25					30		
Pro	Leu	Arg	Val	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val
		35					40					45			
Ser	Leu	Leu	Leu	Ser	Ser	Val	Phe	Trp	Phe	Leu	Val	Arg	Val	Ile	Thr
	50					55					60				
Asp	Asn	Arg	Asp	Gly	Pro	Val	Gln	Asn	Tyr	Leu					
65					70					75					

<210> 172

<211> 79

<212> PRT

<213> Human

<400> 172

Lys	Thr	Ser	Tyr	His	Tyr	His	Thr	Asn	Val	Glu	Glu	Leu	Thr	Ile	Pro
1				5					10					15	
Glu	Thr	Arg	Asn	Asn	Leu	Tyr	Ile	Ser	Ile	Ser	Trp	Leu	Trp	Cys	Leu
			20					25					30		
Val	Leu	Val	Leu	Leu	Ser	Thr	Met	Ile	Leu	Asn	Lys	His	Gly	Trp	Met
		35					40					45			
Lys	Ala	Asn	Ala	Tyr	Ser	Leu	Val	Pro	Ser	Ile	Ile	Tyr	Ser	Pro	Ser
	50					55					60				
Tyr	Leu	Lys	Leu	Leu	Leu	Arg	Leu	Tyr	Lys	Leu	Gln	Ile	Cys	Cys	

1011c2PCTSEQUENCE LISTING

65

70

75

<210> 173
 <211> 134
 <212> PRT
 <213> Human

<220>

<400> 173

Leu	Arg	Gly	Arg	Gly	Arg	Gly	Val	Cys	Ser	Gln	Glu	Ser	Phe	Gly	Gly		
1				5					10					15			
Cys	Cys	Val	Ser	Gly	Leu	Ile	Ala	Met	Gly	Thr	Lys	Ala	Gln	Val	Glu		
			20					25					30				
Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu		
		35				40						45					
Ala	Leu	Gly	Ser	Val	Thr	Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile		
	50				55					60							
Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser		
65					70					75					80		
Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu		
			85						90					95			
Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr		
			100					105					110				
Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr		
		115					120						125				
Gly	Thr	Tyr	Thr	Cys	Met												
	130																

<210> 174
 <211> 137
 <212> PRT
 <213> Human

<400> 174

Ala	Trp	Ser	Arg	Pro	Arg	Tyr	Asp	Ser	Val	Leu	Ala	Leu	Ser	Ala	Ala		
1				5					10					15			
Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Ser	Leu	Val	Leu	Gly	Phe		
			20					25					30				
Leu	Ala	Met	Phe	Val	Ala	Thr	Met	Gly	Met	Lys	Cys	Thr	Arg	Cys	Gly		
		35				40						45					
Gly	Asp	Asp	Lys	Val	Lys	Lys	Ala	Arg	Ile	Ala	Met	Gly	Gly	Gly	Ile		
	50				55					60							
Ile	Phe	Ile	Val	Ala	Gly	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ser	Trp	Tyr		
65				70					75						80		
Gly	His	Gln	Ile	Val	Thr	Asp	Phe	Tyr	Asn	Pro	Leu	Ile	Pro	Thr	Asn		
			85					90					95				
Ile	Lys	Tyr	Glu	Phe	Gly	Pro	Ala	Ile	Phe	Ile	Gly	Trp	Ala	Gly	Ser		
			100				105						110				
Ala	Leu	Val	Ile	Leu	Gly	Gly	Ala	Leu	Ser	Pro	Val	Pro	Val	Leu	Gly		
		115					120						125				
Ile	Arg	Ala	Gly	Leu	Gly	Thr	Cys	Pro									
	130					135											

<210> 175
 <211> 43

1011c2PCTSEQUENCE LISTING

<212> PRT

<213> Human

<400> 175

Met	Lys	Leu	Ser	Gly	Met	Phe	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Phe	Cys
1				5					10					15	
Phe	Leu	Thr	Gly	Val	Phe	Ser	Gln	Gly	Gly	Gln	Val	Asp	Cys	Gly	Glu
			20					25					30		
Ser	Arg	Thr	Pro	Arg	Pro	Thr	Ala	Leu	Gly	Asn					
			35				40								

<210> 176

<211> 63

<212> PRT

<213> Rat

<400> 176

Pro	Asn	Thr	Arg	Pro	Arg	Arg	His	Thr	Ala	Cys	Arg	Val	Ser	Ile	Ser
1				5					10					15	
Val	Phe	Tyr	Met	Leu	His	Thr	Glu	Leu	Lys	Lys	Cys	Trp	Phe	Phe	Leu
			20				25						30		
Phe	Cys	Phe	Ser	Leu	Phe	Leu	Trp	Phe	Cys	Phe	Trp	Phe	Cys	Phe	Leu
			35				40					45			
Leu	Pro	Arg	Phe	Asp	Tyr	Leu	Pro	Met	Pro	Ser	Thr	Arg	Pro	Arg	
	50					55					60				

<210> 177

<211> 52

<212> PRT

<213> mouse

<400> 177

Met	Leu	Gln	Gly	Pro	Ala	Pro	Ser	Cys	Phe	Trp	Val	Phe	Ser	Gly	Ile
1				5					10					15	
Cys	Val	Phe	Trp	Asp	Phe	Ile	Phe	Ile	Ile	Phe	Phe	Asn	Val	Leu	Ser
			20				25					30			
Leu	Gly	Asn	Arg	Glu	Ile	Ser	Ala	Lys	Asp	Phe	Ala	Asp	Gln	Pro	Ala
			35				40					45			
Gly	Ala	Gln	Gly												
	50														

<210> 178

<211> 62

<212> PRT

<213> mouse

<400> 178

Val	Ser	Pro	Arg	Pro	Thr	Tyr	Pro	Ser	Thr	Ala	Ser	Ser	Met	Ala	Ala
1				5					10					15	
Phe	Leu	Val	Thr	Gly	Phe	Phe	Phe	Ser	Leu	Phe	Val	Val	Leu	Gly	Met
			20				25						30		
Glu	Pro	Arg	Ala	Leu	Phe	Arg	Pro	Asp	Lys	Ala	Leu	Pro	Leu	Ser	Cys
			35				40					45			
Ala	Lys	Pro	Thr	Ser	Leu	Cys	Val	Gln	Ser	Ser	Phe	Leu	Gly		
	50					55					60				

1011c2PCTSEQUENCE LISTING

<210> 179
 <211> 123
 <212> PRT
 <213> mouse

<400> 179
 Ala Ser Arg Thr Ala Val Met Ser Leu Cys Arg Cys Gln Gln Gly Ser
 1 5 10 15
 Arg Ser Arg Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly
 20 25 30
 Gly Thr Leu Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu
 35 40 45
 Trp Pro Ser Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr
 50 55 60
 Leu Gly Met Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys
 65 70 75 80
 Tyr Ser Phe Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu
 85 90 95
 His Gly Phe Ser Ala His Lys Gly His Val Ala Gln Arg Gly Gln Val
 100 105 110
 Pro Ser Arg Lys Asn Leu His Phe Gly Cys Val
 115 120

<210> 180
 <211> 120
 <212> PRT
 <213> mouse

<220>
 <221> UNSURE
 <222> (5)...(5)

<400> 180
 Ala Arg Arg Arg Xaa Arg Trp Arg Arg Gly Cys Cys Trp Leu Ile Gly
 1 5 10 15
 Thr Gly Leu Arg Ala Ala Thr Trp Thr Val Leu Cys Ser Pro Asn Ser
 20 25 30
 Ser Leu Val Val Ala Arg His Thr Lys Ser Phe Pro Pro Lys Lys Pro
 35 40 45
 Leu Gln Ala Leu Thr Met Ser Ile Met Asp His Ser Pro Thr Thr Gly
 50 55 60
 Val Val Thr Val Ile Val Ile Leu Ile Ala Ile Ala Ala Leu Gly Gly
 65 70 75 80
 Leu Ile Leu Gly Cys Trp Cys Tyr Leu Arg Leu Gln Arg Ile Ser Gln
 85 90 95
 Ser Glu Asp Glu Glu Ser Ile Val Gly Asp Gly Glu Thr Lys Glu Pro
 100 105 110
 Phe Tyr Trp Cys Ser Thr Leu Leu
 115 120

<210> 181
 <211> 60
 <212> PRT
 <213> mouse

1011c2PCTSEQUENCE LISTING

<400> 181
 Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe
 1 5 10 15
 Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu
 20 25 30
 Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr
 35 40 45
 Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu
 50 55 60

<210> 182
 <211> 72
 <212> PRT
 <213> mouse

<220>

<400> 182
 Lys Pro Thr Val Gly Ser Ala Glu Val Ala Ile Ala Val Phe Leu Val
 1 5 10 15
 Ile Cys Ile Ile Val Val Leu Thr Ile Leu Gly Tyr Cys Phe Phe Lys
 20 25 30
 Asn Gln Arg Lys Glu Phe His Ser Pro Leu His His Pro Pro Pro Thr
 35 40 45
 Pro Ala Ser Ser Thr Val Ser Thr Thr Glu Asp Thr Glu His Leu Val
 50 55 60
 Tyr Asn His Thr Thr Gln Pro Leu
 65 70

<210> 183
 <211> 771
 <212> PRT
 <213> Rat

<220>

<400> 183
 Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu
 1 5 10 15
 Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile
 20 25 30
 Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr
 35 40 45
 Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe
 50 55 60
 Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile
 65 70 75 80
 Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His
 85 90 95
 Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp
 100 105 110
 Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg

1011c2PCTSEQUENCE LISTING

		115					120					125					
Cys	Ala	Gly	Pro	Gly	Glu	Met	Ala	Asp	Lys	Leu	Leu	Leu	Thr	Thr	Pro		
	130					135					140						
Ser	Lys	Asn	Phe	Thr	Cys	Gln	Gly	Pro	Val	Asp	Val	Thr	Ile	Gln	Ala		
145					150					155					160		
Lys	Cys	Asn	Pro	Cys	Leu	Ser	Asn	Pro	Cys	Lys	Asn	Asp	Gly	Thr	Cys		
				165					170					175			
Asn	Asn	Asp	Pro	Val	Asp	Phe	Tyr	Arg	Cys	Thr	Cys	Pro	Tyr	Gly	Phe		
			180					185					190				
Lys	Gly	Gln	Asp	Cys	Asp	Val	Pro	Ile	His	Ala	Cys	Thr	Ser	Asn	Pro		
		195					200					205					
Cys	Lys	His	Gly	Gly	Thr	Cys	His	Leu	Lys	Pro	Arg	Arg	Glu	Thr	Trp		
	210					215					220						
Ile	Trp	Cys	Thr	Cys	Ala	Asp	Gly	Phe	Glu	Gly	Glu	Ser	Cys	Asp	Ile		
225					230					235					240		
Asn	Ile	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	Glu	Asn	Asn	Ser	Thr	Cys		
				245					250					255			
Val	Asp	Gly	Ile	Asn	Asn	Tyr	Thr	Cys	Leu	Cys	Pro	Pro	Glu	Tyr	Thr		
			260					265					270				
Gly	Glu	Leu	Cys	Glu	Glu	Lys	Leu	Asp	Phe	Cys	Ala	Gln	Asp	Leu	Asn		
		275					280					285					
Pro	Cys	Gln	His	Asp	Ser	Lys	Cys	Ile	Leu	Thr	Pro	Lys	Gly	Phe	Lys		
	290					295					300						
Cys	Asp	Cys	Thr	Pro	Gly	Tyr	Ile	Gly	Glu	His	Cys	Asp	Ile	Asp	Phe		
305					310					315					320		
Asp	Asp	Cys	Gln	Asp	Asn	Lys	Cys	Lys	Asn	Gly	Ala	His	Cys	Thr	Asp		
			325					330					335				
Ala	Val	Asn	Gly	Tyr	Thr	Cys	Val	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Leu		
			340					345					350				
Phe	Cys	Glu	Phe	Ser	Pro	Pro	Met	Val	Phe	Leu	Arg	Thr	Ser	Pro	Cys		
	355						360					365					
Asp	Asn	Phe	Asp	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Ile	Arg	Val	Asn		
	370					375					380						
Glu	Pro	Ile	Cys	Gln	Cys	Leu	Pro	Gly	Tyr	Leu	Gly	Glu	Lys	Cys	Glu		
385					390					395					400		
Lys	Leu	Val	Ser	Val	Ser	Ile	Leu	Val	Asn	Lys	Glu	Ser	Tyr	Leu	Gln		
			405						410					415			
Ile	Pro	Ser	Ala	Lys	Val	Arg	Pro	Gln	Thr	Asn	Ile	Thr	Leu	Gln	Ile		
			420					425					430				
Ala	Thr	Asp	Glu	Asp	Ser	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp	Lys	Asp		
	435					440					445						
His	Ile	Ala	Val	Glu	Ser	Ile	Glu	Gly	Ile	Arg	Ala	Ser	Tyr	Asp	Thr		
	450					455					460						
Gly	Ser	His	Pro	Ala	Ser	Ala	Ile	Tyr	Ser	Val	Glu	Thr	Ile	Asn	Asp		
465					470					475					480		
Gly	Asn	Phe	His	Ile	Val	Glu	Leu	Leu	Thr	Leu	Asp	Ser	Ser	Leu	Ser		
			485						490					495			
Leu	Ser	Val	Asp	Gly	Gly	Ser	Pro	Lys	Ile	Ile	Thr	Asn	Leu	Ser	Lys		
			500					505					510				
Gln	Ser	Thr	Leu	Asn	Phe	Asp	Ser	Pro	Leu	Tyr	Val	Gly	Gly	Met	Pro		
		515					520					525					
Gly	Lys	Asn	Asn	Val	Ala	Ser	Leu	Arg	Gln	Ala	Pro	Gly	Gln	Asn	Gly		
	530					535					540						
Thr	Ser	Phe	His	Gly	Cys	Ile	Arg	Asn	Leu	Tyr	Ile	Asn	Ser	Glu	Leu		
545					550					555					560		

1011c2PCTSEQUENCE LISTING

Gln	Asp	Phe	Arg	Lys	Val	Pro	Met	Gln	Thr	Gly	Ile	Leu	Pro	Gly	Cys	
				565					570					575		
Glu	Pro	Cys	His	Lys	Lys	Val	Cys	Ala	His	Gly	Thr	Cys	Gln	Pro	Ser	
			580					585					590			
Ser	Gln	Ser	Gly	Phe	Thr	Cys	Glu	Cys	Glu	Glu	Gly	Trp	Met	Gly	Pro	
		595					600					605				
Leu	Cys	Asp	Gln	Arg	Thr	Asn	Asp	Pro	Cys	Leu	Gly	Asn	Lys	Cys	Val	
	610					615					620					
His	Gly	Thr	Cys	Leu	Pro	Ile	Asn	Ala	Phe	Ser	Tyr	Ser	Cys	Lys	Cys	
625					630					635					640	
Leu	Glu	Gly	His	Gly	Gly	Val	Leu	Cys	Asp	Glu	Glu	Glu	Asp	Leu	Phe	
			645						650					655		
Asn	Pro	Leu	Pro	Gly	Asp	Gln	Val	Gln	Ala	Arg	Glu	Val	Gln	Ala	Leu	
		660						665					670			
Trp	Ala	Arg	Ala	Ala	Leu	Leu	Trp	Met	Gln	Gln	Trp	Ile	His	Arg	Gly	
		675					680					685				
Gln	Leu	Thr	Gln	Arg	Ile	Ser	Cys	Arg	Gly	Glu	Arg	Ile	Arg	Asp	Tyr	
	690					695					700					
Tyr	Gln	Ser	Ser	Arg	Val	Arg	Cys	Leu	Ser	Asn	Asp					

<210> 184
 <211> 340
 <212> PRT
 <213> mouse

<400> 184

Asp	Gly	Ser	Leu	Trp	Leu	Gln	Ala	Thr	Gln	Pro	Asp	Asp	Ala	Gly	His	
1				5					10					15		
Tyr	Thr	Cys	Val	Pro	Ser	Asn	Gly	Phe	Leu	His	Pro	Pro	Ser	Ala	Ser	
			20					25					30			
Ala	Tyr	Leu	Thr	Val	Leu	Tyr	Pro	Ala	Gln	Val	Thr	Val	Met	Pro	Pro	
		35					40					45				
Glu	Thr	Pro	Leu	Pro	Thr	Gly	Met	Arg	Gly	Val	Ile	Arg	Cys	Pro	Val	
	50					55					60					
Arg	Ala	Asn	Pro	Pro	Leu	Leu	Phe	Val	Thr	Trp	Thr	Lys	Asp	Gly	Gln	
65					70					75					80	
Ala	Leu	Gln	Leu	Asp	Lys	Phe	Pro	Gly	Trp	Ser	Leu	Gly	Pro	Glu	Gly	
			85						90					95		
Ser	Leu	Ile	Ile	Ala	Leu	Gly	Asn	Glu	Asp	Ala	Leu	Gly	Glu	Tyr	Ser	
		100						105					110			
Cys	Thr	Pro	Tyr	Asn	Ser	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Pro	Val	Thr	
		115					120					125				
Arg	Val	Leu	Leu	Lys	Ala	Pro	Pro	Ala	Phe	Ile	Asp	Gln	Pro	Lys	Glu	
	130					135					140					
Glu	Tyr	Phe	Gln	Glu	Val	Gly	Arg	Glu	Leu	Leu	Ile	Pro	Cys	Ser	Ala	
145					150					155					160	
Arg	Gly	Asp	Pro	Pro	Ile	Val	Ser	Trp	Ala	Lys	Val	Gly	Arg	Gly		
			165					170						175		
Leu	Gln	Gly	Gln	Ala	Gln	Val	Asp	Ser	Asn	Asn	Ser	Leu	Val	Leu	Arg	
			180					185					190			
Pro	Leu	Thr	Lys	Glu	Ala	Gln	Gly	Arg	Trp	Glu	Cys	Ser	Ala	Ser	Asn	
		195					200					205				
Ala	Val	Ala	Arg	Val	Thr	Thr	Ser	Thr	Asn	Val	Tyr	Val	Leu	Gly	Thr	
	210					215					220					
Ser	Pro	His	Val	Val	Thr	Asn	Val	Ser	Val	Val	Pro	Leu	Pro	Lys	Gly	

1011c2PCTSEQUENCE LISTING

225					230					235					240
Ala	Asn	Val	Ser	Trp	Glu	Pro	Gly	Phe	Asp	Gly	Gly	Tyr	Leu	Gln	Arg
				245					250					255	
Phe	Ser	Val	Trp	Tyr	Thr	Pro	Leu	Ala	Lys	Arg	Pro	Asp	Arg	Ala	His
			260					265					270		
His	Asp	Trp	Val	Ser	Leu	Ala	Val	Pro	Ile	Gly	Ala	Thr	His	Leu	Leu
		275					280					285			
Val	Pro	Gly	Leu	Gln	Ala	His	Ala	Gln	Tyr	Gln	Phe	Ser	Val	Leu	Ala
	290					295					300				
Gln	Asn	Lys	Leu	Gly	Ser	Gly	Pro	Phe	Ser	Glu	Ile	Val	Leu	Ser	Ile
305					310					315				320	
Pro	Glu	Gly	Leu	Pro	Thr	Thr	Pro	Ala	Ala	Pro	Gly	Leu	Pro	Ala	Thr
				325					330					335	
Arg	Ser	Arg	Val												
			340												

<210> 185
 <211> 536
 <212> PRT
 <213> mouse

<400> 185

Lys	Val	Glu	Gly	Glu	Gly	Arg	Gly	Arg	Trp	Ala	Leu	Gly	Leu	Leu	Arg
1				5					10					15	
Thr	Phe	Asp	Ala	Gly	Glu	Phe	Ala	Gly	Trp	Glu	Lys	Val	Gly	Ser	Gly
			20					25					30		
Gly	Phe	Gly	Gln	Val	Tyr	Lys	Val	Arg	His	Val	His	Trp	Lys	Thr	Trp
		35					40					45			
Leu	Ala	Ile	Lys	Cys	Ser	Pro	Ser	Leu	His	Val	Asp	Asp	Arg	Glu	Arg
	50					55					60				
Met	Glu	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Met	Glu	Met	Ala	Lys	Phe	Arg
65				70						75					80
Tyr	Ile	Leu	Pro	Val	Tyr	Gly	Ile	Cys	Gln	Glu	Pro	Val	Gly	Leu	Val
			85						90					95	
Met	Glu	Tyr	Met	Glu	Thr	Gly	Ser	Leu	Glu	Lys	Leu	Leu	Ala	Ser	Glu
			100					105					110		
Pro	Leu	Pro	Trp	Asp	Leu	Arg	Phe	Arg	Ile	Val	His	Glu	Thr	Ala	Val
		115					120					125			
Gly	Met	Asn	Phe	Leu	His	Cys	Met	Ser	Pro	Pro	Leu	Leu	His	Leu	Asp
	130					135					140				
Leu	Lys	Pro	Ala	Asn	Ile	Leu	Leu	Asp	Ala	His	Tyr	Gln	Met	Ser	Arg
145				150						155					160
Phe	Leu	Asp	Phe	Gly	Leu	Ala	Lys	Cys	Asn	Gly	Met	Ser	His	Ser	His
			165						170					175	
Asp	Leu	Ser	Met	Asp	Gly	Leu	Phe	Gly	Thr	Ile	Gly	Tyr	Leu	Pro	Pro
			180					185					190		
Glu	Arg	Ile	Arg	Glu	Lys	Ser	Arg	Leu	Phe	Asp	Thr	Lys	His	Asp	Val
		195					200					205			
Tyr	Ser	Phe	Ala	Ile	Val	Ile	Trp	Gly	Val	Leu	Thr	Gln	Asn	Asn	Pro
	210					215					220				
Phe	Ala	Asp	Glu	Lys	Asn	Ile	Leu	His	Ile	Met	Met	Lys	Val	Val	Lys
225					230					235					240
Gly	His	Arg	Pro	Glu	Leu	Pro	Pro	Ile	Cys	Arg	Pro	Arg	Pro	Arg	Ala
				245					250					255	
Cys	Ala	Ser	Leu	Ile	Gly	Leu	Met	Gln	Arg	Cys	Trp	His	Ala	Asp	Pro

1011c2PCTSEQUENCE LISTING

			260					265					270				
Gln	Val	Arg	Pro	Thr	Phe	Gln	Glu	Ile	Thr	Ser	Glu	Thr	Glu	Asp	Leu		
		275					280					285					
Cys	Glu	Lys	Pro	Asp	Glu	Glu	Val	Lys	Asp	Leu	Ala	His	Glu	Pro	Gly		
	290					295					300						
Glu	Lys	Ser	Ser	Leu	Glu	Ser	Lys	Ser	Glu	Ala	Arg	Pro	Glu	Ser	Ser		
305					310					315					320		
Arg	Leu	Lys	Arg	Ala	Ser	Ala	Pro	Pro	Phe	Asp	Asn	Asp	Cys	Ser	Leu		
			325						330					335			
Ser	Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Ile	Phe	Pro	Arg	Leu	Leu		
		340						345					350				
Lys	Gly	Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Ser	Glu	Cys	Lys	Leu	Pro		
	355					360						365					
Ser	Ser	Ser	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser		
370					375						380						
Ala	Phe	Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Ala		
385					390					395					400		
Ser	Thr	Gly	Asp	Leu	Gly	Pro	Thr	Asp	Ile	Gln	Lys	Lys	Lys	Leu	Val		
			405					410						415			
Asp	Ala	Ile	Ile	Ser	Gly	Asp	Thr	Ser	Arg	Leu	Met	Lys	Ile	Leu	Gln		
		420						425					430				
Pro	Gln	Asp	Val	Asp	Leu	Val	Leu	Asp	Ser	Ser	Ala	Ser	Leu	Leu	His		
	435					440						445					
Leu	Ala	Val	Glu	Ala	Gly	Gln	Glu	Glu	Cys	Val	Lys	Trp	Leu	Leu	Leu		
450					455					460							
Asn	Asn	Ala	Asn	Pro	Asn	Leu	Thr	Asn	Arg	Lys	Gly	Ser	Thr	Pro	Leu		
465					470					475					480		
His	Met	Ala	Val	Glu	Arg	Lys	Gly	Arg	Gly	Ile	Val	Glu	Leu	Leu	Leu		
			485					490						495			
Ala	Arg	Lys	Thr	Ser	Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala		
		500						505					510				
Leu	His	Phe	Ala	Ala	Gln	Asn	Gly	Asp	Glu	Gly	Gln	His	Lys	Ala	Ala		
	515					520					525						
Ala	Arg	Glu	Glu	Cys	Phe	Cys	Gln										
530						535											

<210> 186

<211> 337

<212> PRT

<213> Rat

<220>

<400> 186

Arg	Phe	Gly	Tyr	Gln	Met	Asp	Glu	Gly	Asn	Gln	Cys	Val	Asp				
1				5				10				15					
Val	Asp	Glu	Cys	Ala	Thr	Asp	Ser	His	Gln	Cys	Asn	Pro	Thr	Gln	Ile		
		20						25				30					
Cys	Ile	Asn	Thr	Glu	Gly	Gly	Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr		
	35					40					45						
Trp	Leu	Leu	Glu	Gly	Gln	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly		
50					55					60							
Tyr	Cys	Gln	Gln	Leu	Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr		
65					70					75					80		

1011c2PCTSEQUENCE LISTING

Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
 85 90 95
 Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
 100 105 110
 Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
 115 120 125
 Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
 130 135 140
 Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
 145 150 155 160
 Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
 165 170 175
 Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
 180 185 190
 Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
 195 200 205
 Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
 210 215 220
 Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
 225 230 235 240
 Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
 245 250 255
 Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
 260 265 270
 Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
 275 280 285
 Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
 290 295 300
 Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
 305 310 315 320
 Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
 325 330 335
 Phe

<210> 187
 <211> 152
 <212> PRT
 <213> mouse

<400> 187
 Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met
 1 5 10 15
 Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala
 20 25 30
 Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu
 35 40 45
 Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn
 50 55 60
 Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln
 65 70 75 80
 Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His
 85 90 95
 Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala
 100 105 110

1011c2PCTSEQUENCE LISTING

Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe
 115 120 125
 Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile
 130 135 140
 Ile Cys Ser Gly Gly Ser Pro Leu
 145 150

<210> 188

<211> 118

<212> PRT

<213> Rat

<220>

<400> 188

Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr ThrAla Tyr Asp Arg
 1 5 10 15
 Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg
 20 25 30
 Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser
 35 40 45
 Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly
 50 55 60
 Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg
 65 70 75 80
 Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val
 85 90 95
 Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln
 100 105 110
 Arg Leu Leu Ile Val Ser
 115

<210> 189

<211> 299

<212> PRT

<213> Human

<220>

<400> 189

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

1011c2PCTSEQUENCE LISTING

115	120	125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr		
130	135	140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro		
145	150	155
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn		
165	170	175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro		
180	185	190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly		
195	200	205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser		
210	215	220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val		
225	230	235
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly		
245	250	255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly		
260	265	270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu		
275	280	285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val		
290	295	

<210> 190
 <211> 91
 <212> PRT
 <213> Human

<400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
1 5 10 15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
20 25 30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
35 40 45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
50 55 60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
65 70 75 80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
85 90

<210> 191
 <211> 89
 <212> PRT
 <213> mouse

<400> 191
Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp
1 5 10 15
Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys
20 25 30
Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala
35 40 45

1011c2PCTSEQUENCE LISTING

Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro
 50 55 60
 Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro
 65 70 75 80
 Cys Gln Pro Gly Gln Arg Val Glu Val
 85

<210> 192
 <211> 299
 <212> PRT
 <213> mouse

<220>

<400> 192
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
 1 5 10 15
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
 20 25 30
 Val Cys Thr Cys Gly Gln Gly Ala Cys Asp Pro Val Ser Gly Thr
 35 40 45
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
 50 55 60
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
 65 70 75 80
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
 85 90 95
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
 100 105 110
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
 115 120 125
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
 130 135 140
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
 145 150 155 160
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
 165 170 175
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
 180 185 190
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
 195 200 205
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
 210 215 220
 Pro Gly Arg Ala Gly Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
 225 230 235 240
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
 245 250 255
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
 260 265 270
 Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
 275 280 285
 Pro Gln His Ser Ser Ser Lys Ala Met Lys His
 290 295

1011c2PCTSEQUENCE LISTING

<210> 193
 <211> 314
 <212> PRT
 <213> mouse

<220>

<400> 193

Glu	Glu	Pro	Cys	Asn	Asn	Gly	Ser	Glu	Ile	Leu	Ala	Tyr	Asn	Ile	Asp
1				5				10						15	
Leu	Gly	Asp	Ser	Cys	Ile	Thr	Val	Gly	Asn	Thr	Thr	Thr	His	Val	Met
			20					25					30		
Lys	Asn	Leu	Leu	Pro	Glu	Thr	Thr	Tyr	Arg	Ile	Arg	Ile	Gln	Ala	Ile
		35				40					45				
Asn	Glu	Ile	Gly	Val	Gly	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Lys	Thr
	50				55					60					
Arg	Pro	Leu	Pro	Pro	Ser	Pro	Pro	Arg	Leu	Glu	Cys	Ala	Ala	Ser	Gly
65					70					75					80
Pro	Gln	Ser	Leu	Lys	Leu	Lys	Trp	Gly	Asp	Ser	Asn	Ser	Lys	Thr	His
				85				90						95	
Ala	Ala	Gly	Asp	Met	Val	Tyr	Thr	Leu	Gln	Leu	Glu	Asp	Arg	Asn	Lys
			100					105					110		
Arg	Phe	Ile	Ser	Ile	Tyr	Arg	Gly	Pro	Ser	His	Thr	Tyr	Lys	Val	Gln
		115					120					125			
Arg	Leu	Thr	Glu	Phe	Thr	Cys	Tyr	Ser	Phe	Arg	Ile	Gln	Ala	Met	Ser
	130				135						140				
Glu	Ala	Gly	Glu	Gly	Pro	Tyr	Ser	Glu	Thr	Tyr	Thr	Phe	Ser	Thr	Thr
145				150						155					160
Lys	Ser	Val	Pro	Pro	Thr	Leu	Lys	Ala	Pro	Arg	Val	Thr	Gln	Leu	Glu
				165				170						175	
Gly	Asn	Ser	Cys	Glu	Ile	Phe	Trp	Glu	Thr	Val	Pro	Pro	Met	Arg	Gly
			180					185					190		
Asp	Pro	Val	Ser	Tyr	Val	Leu	Gln	Val	Leu	Val	Gly	Arg	Asp	Ser	Glu
		195					200				205				
Tyr	Lys	Gln	Val	Tyr	Lys	Gly	Glu	Glu	Ala	Thr	Phe	Gln	Ile	Ser	Gly
	210				215					220					
Leu	Gln	Ser	Asn	Thr	Asp	Tyr	Arg	Phe	Arg	Val	Cys	Ala	Cys	Arg	Arg
225				230						235					240
Cys	Val	Asp	Thr	Ser	Gln	Glu	Leu	Ser	Gly	Ala	Phe	Ser	Pro	Ser	Ala
				245				250						255	
Ala	Phe	Met	Leu	Gln	Gln	Arg	Glu	Val	Met	Leu	Thr	Gly	Asp	Leu	Gly
			260					265					270		
Gly	Met	Glu	Glu	Ala	Lys	Met	Lys	Gly	Met	Met	Pro	Thr	Asp	Glu	Gln
		275				280					285				
Phe	Ala	Ala	Leu	Ile	Val	Leu	Gly	Phe	Ala	Thr	Leu	Ser	Ile	Leu	Phe
	290				295					300					
Ala	Phe	Ile	Leu	Gln	Tyr	Phe	Leu	Met	Lys						
305				310											

<210> 194
 <211> 109
 <212> PRT
 <213> mouse

<400> 194

Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His

1011c2PCTSEQUENCE LISTING

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Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu			
20	25	30	
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met			
35	40	45	
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro			
50	55	60	
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile			
65	70	75	80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr			
85	90	95	
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr			
100	105		

<210> 195
 <211> 237
 <212> PRT
 <213> mouse

<400> 195
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
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20 25 30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
35 40 45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
50 55 60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65 70 75 80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
85 90 95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100 105 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115 120 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130 135 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145 150 155 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165 170 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180 185 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195 200 205
Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
210 215 220
His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
225 230 235

<210> 196
 <211> 154
 <212> PRT
 <213> Human

1011c2PCTSEQUENCE LISTING

<400> 196
 Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1 5 10 15
 Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
 20 25 30
 Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile
 35 40 45
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
 50 55 60
 Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
 65 70 75 80
 Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu
 85 90 95
 His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile
 100 105 110
 Ala Ile Gly Ile Gly Val Gly Leu Leu Leu Ser Gly Phe Leu Val Ile
 115 120 125
 Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr
 130 135 140
 Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
 145 150

<210> 197
 <211> 171
 <212> PRT
 <213> Rat

<400> 197
 Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu
 1 5 10 15
 Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln
 20 25 30
 Met Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr Glu
 35 40 45
 Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr
 50 55 60
 Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe
 65 70 75 80
 Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser
 85 90 95
 Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp
 100 105 110
 Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe
 115 120 125
 Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg
 130 135 140
 Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu
 145 150 155 160
 Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
 165 170

<210> 198
 <211> 1399
 <212> DNA

1011c2PCTSEQUENCE LISTING

<213> Mouse

<400> 198

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120
ggagaccaca ggtgctaagt gaggggtgctc acagaacccc ctcttcagcc agagatcact
180
agcaggggaa ctgtggagaa ggcagccagc aaggaagagc ctgagagtag cctccatggg
240
cttggaagccc agctggatatc tgctgctctg tttggctgctc tctggggcag cagggactga
300
ccctcccaca gcgcccacca cagcagaaag acagcggcag cccacggaca tcattcttaga
360
ctgcttcttg gtgacagaag acaggcaccg cggggctttt gccagcagtg gggacagggg
420
gagggccttg cttgtgctga agcaggtacc agtgctggat gatggctccc tgggaaggcat
480
cacagatttc caggggagca ctgagaccaa acaggattca cctgttatct ttgaggcctc
540
agtggacttg gtacagattc cccaggcaga ggcgttgctc catgctgact gcagcgggaa
600
ggcagtgacc tgcgagatct ccaagtattt cctccaggcc agacaagagg ccacttttga
660
gaaagcacat tggttcatca gcaacatgca ggtttctaga ggtggcccca gtgtctccat
720
ggtgatgaag actctaagag atgctgaagt tggagctgctc cggcacccta cactgaacct
780
acctctgagt gcccagggca cagtgaagac tcaagtggag ttccagggtga catcagagac
840
ccaaaccctg aaccacctgc tggggctctc tgtctccctg cactgcagtt tctccatggc
900
accagacctg gacctcactg gcgtggagtg gcggctgcag cataaaggca gcggccagct
960
ggtgtacagc tggaagacag ggcaggggca ggccaagcgc aagggcgcta cactggagcc
1020
tgaggagcta ctcagggctg gaaacgcctc tctcacctta cccaacctca ctctaaagga
1080
tgaggggacc tacatctgcc agatctccac ctctctgtat caagctcaac agatcatgcc
1140
acttaacatc ctggctcccc ccaaagtaca actgcacttg gcaaacaagg atcctctgcc
1200
ttccctcgtc tgcagcattg ccggctacta tcctctggat gtgggagtga cgtggattcg
1260
agaggagctg ggtggaattc cagcccaagt ctctggtgcc tccttctcca gcctcaggca
1320
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1380
tgccacttat acctgcaa
1399

<210> 199

<211> 469

<212> DNA

1011c2PCTSEQUENCE LISTING

<213> Rat

<400> 199

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cacggtgctc ggagcgctgg gcaccctggg cagcgagttt ctgcgggagt gggagacaca
120
agatatgcga gtgactctct tcaagcttct cctgcttttg ttggtgttaa gtctcctggg
180
catccagctg gcgtgggggt tctacgggaa cacagtgacc gggttgtatc accgtccagg
240
gaaatggcag caaatgaagc tctcaaaact cacagagaat aaaggaaggc agcaggagaa
300
gggtctccag agatatcgct gggctctgctg gctcctgtgc tgtaccttgc tgctatccag
360
accccttagg caactgcaga gggcttgggt tgggggactg gagtaccatg atgctcccag
420
ggtgagcctc cactgccttc agccttgctt ccaacagcgt caggtactg
469

```

<210> 200

<211> 529

<212> DNA

<213> Rat

<400> 200

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aaagcttcca tcctcaacat gccactagtg acgacactct tctacgcctg cttctatcac
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tacacggagt ccgaggggac cttcagcagt ccagtcaacc tgaagaaaac attcaagatc
120
ccagacagac agtatgtgct gacagccttg gctgcgcggg ccaagcttag agcctggaat
180
gatgtcgacg ccttggtcac cacaagaac tggttgggtt acaccaagaa gagagcaccc
240
attggcttcc atcgagttgt ggaaattttg cacaagaaca gtgcccctgt ccagatattg
300
caggaatatg tcaatctggt ggaagatgtg gacacaaagt tgaacttagc cactaagttc
360
aagtgccatg atgttgatc tgaacttgc cgagacctga aggatcgtca acagttgctt
420
gcatacagga gcaaagtaga taaaggatct gctgaggaag agaaaatcga tgtcatcctc
480
agcagctcgc aaattcgatg gaagaactaa gggtcttttg ctaccaga
529

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<210> 201

<211> 1230

<212> DNA

<213> Rat

<400> 201

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aagaattcgg cacgaggcca tggctgggtg ggcggggggc gagctctcgg tcctgaaccc
60
gctgcgtgcg ctgtggctgt tgctggccgc cgccttcctg ctgcactgc tgctgcagct
120

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1011c2PCTSEQUENCE LISTING

ggcgcccgcc aggctgctac cgagctgcgc gctcttccag gacctcatcc gctacgggaa
 180
 gaccaagcag tccggctcgc ggcgccccgc cgtctgcagg gccttcgacg tccccaagag
 240
 gtacttttct cacttctacg tcgtctcagt gttatggaat ggctccctgc tctggttcct
 300
 gtctcagtct ctgttctcgg gagcgccggt tccaagctgg ctttgggctt tgctcagaac
 360
 tcttggggtc acgcagttcc aagccctggg gatggagtcc aaggcttctc ggatacaagc
 420
 aggcgagctg gctctgtcta ccttcttagt gttgggtgttc ctctgggtcc atagtcttcg
 480
 gagactcttc gagtgccttct acgtcagcgt cttctctaac acggccattc acgtcgtgca
 540
 gtactgtttc gggctgggtct actatgtcct tgttggcctg accgtactga gccaagtgcc
 600
 catgaatgac aagaacgtgt acgctctggg gaagaatcta ctgctacaag ctcggtgggt
 660
 ccacatcttg ggaatgatga tgttcttctg gtcctctgcc catcagtata agtgccacgt
 720
 cattctcagc aatctcagga gaaataagaa aggtgtggtc atccactgcc agcacagaat
 780
 cccctttgga gactggttcg agtatgtgtc ttctgctaac tacctagcag agctgatgat
 840
 ctacatctcc atggctgtca ccttcgggct ccacaacgta acctgggtggc tgggtggtgac
 900
 ctatgtcttc ttcagccaag ccttgtctgc gttcttcaac cacaggttct acaaaagcac
 960
 atttgtgtcc tacccaaagc ataggaaagc ttctctcccg ttcttggttt gaacaggctt
 1020
 tatgggtgaag agcgcagccc aggtgacagg ttcccttctc cgagacgctg agacaggctg
 1080
 aagtacactt tctgcagctg gcgcccccca ggctgctacc gagctgcgcg ctcttccagg
 1140
 acctcatccg ctacgggaag accaagcagt ccggctcgcg gcgccccgcc gtctgcagcc
 1200
 cgggggatcc actagttcta gagcgccgcc
 1230

<210> 202

<211> 778

<212> DNA

<213> Rat

<400> 202

ctgcaggctg acactagtgg atccaaagat tcggcagcag ataaggcaca ttgcttcat
 60
 aaaataaaaa aaaaggaaat ttacttagcc gcatgtcagt cacccaaatt ttgagtgtac
 120
 aatgaaatg gaaaacattt attacacaaa tttaattaca attctaggga ataaacatgc
 180
 aatcagatg gagtcaatc tgcaggcgct gatectctcc ccttgggttg cagtctgtgc
 240
 acctcttggg ttcgccccgc accaggcagt cagaggcctg gctcttgacg gcaggaggat
 300

1011c2PCTSEQUENCE LISTING

cactgttgta aagaacagcg tcacatttag cgcattctggc gtagtagcag tttttaacac
 360
 tttgcgcagg tgcctccctt cccccaccgc cgcttttgta ggtctacctc tctaaatctc
 420
 tgccttcctc gcacagtaag tgacctctcc atgacaaagg gccccagac agcagttata
 480
 aatcaatgtg ttttgggttt gtttgtttgt ttgttttggt ttaaagaaaa acccggccat
 540
 gcttggtggc acttgccctt aatagtagcg cttggtagac agaggcaagc ggttctctgt
 600
 aagttcaagg ccagcctggc ctacacagtg agaccgggtc tcaaaaacaa aacaacaaaa
 660
 aacaactcct attgaatcca ctacaggaag ggggggcgcg gatcactgtc tgcaaaactaa
 720
 agtgacttga gctcctgtca cagcctttcc agcaagggca agcttcttta ttagttat
 778

<210> 203
 <211> 1123
 <212> DNA
 <213> Rat

<400> 203
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 120
 cgggtgccta cagcccccat cagcttcccc ggggagattc tgccgatttg tcacgagcca
 180
 tgctcaggag gcagctcgtc tgggtggcacc tgctggcttt gcttttcctc ccattttgcc
 240
 tgtgtcaaga tgaatacatg gagtctccac aagctggagg actgccccca gactgcagca
 300
 agtgttgcc aaggagattat ggattccgtg gttaccaagg gccccctgga cccccaggtc
 360
 ctctggcat tccaggaaac catggaaaca atggaaataa cggagccact ggccacgaag
 420
 gggccaaggg tgagaaagga gacaaaggcg acctggggcc tcgaggggaa cgggggcagc
 480
 atggcccaa aggatagaag ggatacccag gggtgccacc agagctgcag attgcgttca
 540
 tggcttctct agcgactcac ttcagcaatc agaacagtgg cattatcttc agcagtgttg
 600
 agaccaacat tggaacttc ttcgatgtca tgactggtag atttggggcc ccgatatcag
 660
 gcgtgtattt cttcaccttc agcatgatga agcatgagga cgtggaggaa gtgtatgtgt
 720
 accttatgca caatggtaac acggtgttca gcatgtacag ctatgaaaca aagggaaaat
 780
 cagatacatc cagcaaccat gcagtgtga agttggccaa aggagatgaa gtctggctaa
 840
 gaatgggcaa cggtgccctc catggggacc accagcgctt ctctaccttc gcaggctttc
 900
 tgctttttga aactaagtga tgaggaagtc aggatagctc catgctaagg gcgatttgta
 960

1011c2PCTSEQUENCE LISTING

ggtgagctag ggttgtagg atctgagggg tgttgagtt gggcttctct atggagtatt
 1020
 taactgttac attggtcaca ctgctactca ttctaattggc ataccaatta tgttggtatc
 1080
 tttaggggct aggaagaata gaccacaagg taatattccc aga
 1123

<210> 204
 <211> 434
 <212> DNA
 <213> Mouse

<400> 204
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 60
 attgttaaaa aattgacatc agaaatattt acagaaatag atacctgttt gaataaagtt
 120
 agagatgaaa tttttgctaa acttcaaccg aagcttagat gcacattagg tgacatggaa
 180
 agtctgtgtg ttgcacttcc tgtactgtta aagcttgaac cccatgttga aagcctcttt
 240
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 300
 tgtgtgaaga gtctgggtcac ctttaccaat attgttcctg agtggcatcc actcaatgct
 360
 gcccatcttg gtccatgtaa cagctgcaac agtaaatcac aaataagaaa aatgggtgttg
 420
 gaaagagcgt cgcc
 434

<210> 205
 <211> 783
 <212> DNA
 <213> Mouse

<400> 205
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 ggttgcgggc tcgcgcctgc cacgggtcat cagccagcag agtgtgtgtc gtgcaaggcc
 120
 catctggtgg ggaacacagc gccggggctc ggagaccatg gcgggcgctg cgggtgaagta
 180
 cttaagtcag gaggaggctc aggccgtgga ccaagagctt tttaacgagt atcagttcag
 240
 cgtggatcaa ctcatggagc tggccgggtt gagctgtgcc acggctattg ccaaggctta
 300
 tccccccacg tctatgtcca agagtcccc gactgtcttg gtcatctgtg gccccggaaa
 360
 taacggaggg gatgggctgg tctgtgcgcg acacctcaaa ctttttggtt accagccaac
 420
 tatctattac cccaaaagac ctaacaagcc cctcttcact gggctagtga ctcagtgtca
 480
 gaaaatggac attcctttcc ttgggtgaaat gccccagag gatgggatgt agagaaggga
 540
 aaccctagcg gaatccaacc agacttactc atctcactga cggcacccaa gaagtctgca

1011c2PCTSEQUENCE LISTING

600
 actcacttta ctggccgata tcattacctt ggggggtcgct ttgtaccacc tgctctagag
 660
 aagaagtacc agctgaacct gccatcttac cctgacacag agtgtgtcta ccgtctacag
 720
 taagggaggt gggtaggcag gattctcaat aaagacttgg tactttctgt cttgaaaaaa
 780
 aaa
 783

<210> 206
 <211> 480
 <212> DNA
 <213> Mouse

<400> 206
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 tagtaacaag ataccatgca gctccctcta gcctcggatc accgaagcag gaagaaggtc
 180
 agactgcccc catcccagat ttgcttagtt tgtctcccaa tgtgctggac tttaaagaca
 240
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 300
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 360
 gatcatcatt acaatggacc aactgagggg tgccttcata ttagaccaat taaaagttgc
 420
 tgtgagttaa accaggaatg accgcacttc cacatcagaa atcaaacaaa atcaatgggt
 480

<210> 207
 <211> 501
 <212> DNA
 <213> Mouse

<400> 207
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 120
 cagcatcggt cttatatgcg actaacagaa aaggaagatg aatcattacc aatagatata
 180
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 240
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 300
 aatcacccat ctttttatgt gtttaaccat cgtggctcag tgctgttccg gccttcagat
 360
 gcaacaaatt cttcaaacct agatgcattg tcctctaata catcgttgaa gttacgaaag
 420
 tttgactcac tgcgccgtta agctttttac aaattaaata acaggacaga cacagaattg
 480

1011c2PCTSEQUENCE LISTING

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501

<210> 208
<211> 480
<212> DNA
<213> Mouse

<400> 208
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120
tggctttcct ttttagtttt tttacttttt agtttagttt gttcttttcc ttccccaata
180
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240
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300
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360
ctgttgcttt tgcattgtta atatagacgt tcctgtcgat ccttgggaga tcatggcctt
420
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480

<210> 209
<211> 962
<212> DNA
<213> Mouse

<400> 209
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120
aatgatgcc acagaaatcc tttattcaca tgtgggttaa cctgtcccgg cacaccccag
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240
ggatcgaaac agtcgagttc aagtgggctg cagggaactg cggtcacca aatacatttc
300
ggacggccag tgcaccagca tcagccctct gaaggagctg gtgtgcgcgg gcgagtgtt
360
gccctgccg gtgcttccca actggatcgg aggaggctac ggaacaaagt actggagccg
420
gaggagctct caggagtggc ggtgtgtcaa cgacaagacg cgcaccaga ggatccagct
480
gcagtgtcag gacggcagca cgcgcaccta caaatcacc gtggtcacgg cgtgcaagt
540
caagaggtag acccgtcagc acaacgagtc cagccacaac tttgaaagcg tgtcgccagc
600
caagcccggc cagcaccaca gagagcggaa gagagccagc aaatccagca agcacagtct
660
gagctagacc tggactgact aggaagcatc tgctaccag atttgattgc ttggaagact

1011c2PCTSEQUENCE LISTING

720
ctctctcgag cctgccattg ctctttcttc acttgaaagt atatgctttc tgctttgatc
780
aagcccagca ggctgtcctt ctctgggact agcttttctt ttgcaagtgt ctcaagatgt
840
aatgagtggg ttgcagtgaag agccaggcat cctgtagttt ccatccccct ccccatccca
900
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960

aa

962

<210> 210
<211> 778
<212> DNA
<213> Mouse

<400> 210
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cgggctcgcg cctgccacgg gtcacagcc agcagagtgt gtgtcgtgca aggcccatct
120
ggtggggaac acagcgccgg ggctcggaga ccatggcggg cgctgcggtg aagtacttaa
180
gtcaggagga ggctcaggcc gtggaccaag agctttttta cgagtatcag ttcagcgtgg
240
atcaactcat ggagctggcc gggttgagct gtgccacggc tattgccaag gcttatcccc
300
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360
gaggggatgg gctgggtctgt gcgcgacacc tcaaactttt tggttaccag ccaactatct
420
attaccccaa aagacctaac aagccctct tcaactgggt agtgactcag tgtcagaaaa
480
tggaattcc tttccttggg gaaatgcccc cagaggatgg gatgtagaga agggaaaccc
540
tagcggaaac caaccagact tactcatctc actgacggca cccaagaagt ctgcaactca
600
ctttactggc cgatatcatt accttggggg tcgctttgta ccacctgctc tagagaagaa
660
gtaccagctg aacctgccat cttaccctga cacagagtgt gtctaccgtc tacagtaagg
720
gaggtgggta ggcaggattc tcaataaaga cttggtactt tctgtcttga aaaaaaaa
778

<210> 211
<211> 1152
<212> DNA
<213> Mouse

<400> 211
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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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1320

1011c2PCTSEQUENCE LISTING

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 <213> Rat

<400> 214

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1011c2PCTSEQUENCE LISTING

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<211> 493
<212> DNA
<213> Mouse

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<211> 511
<212> DNA
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1011c2PCTSEQUENCE LISTING

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 <211> 1107
 <212> DNA
 <213> Rat

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Rat

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<210> 219
 <211> 2206
 <212> DNA
 <213> Rat

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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 <211> 376
 <212> DNA
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 <212> DNA
 <213> Human

<400> 221
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1011c2PCTSEQUENCE LISTING

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 420
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 <211> 550
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 <213> Mouse

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<210> 224

1011c2PCTSEQUENCE LISTING

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<212> DNA

<213> Mouse

<400> 224

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<211> 1752

<212> DNA

<213> Rat

<400> 225

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1011c2PCTSEQUENCE LISTING

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 <211> 2165
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 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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2165

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<211> 1348

<212> DNA

<213> Mouse

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<221> unsure

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1011c2PCTSEQUENCE LISTING

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 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Rat

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<400> 229

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1011c2PCTSEQUENCE LISTING

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<211> 2004

1011c2PCTSEQUENCE LISTING

<212> DNA

<213> Rat

<400> 230

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1440
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1011c2PCTSEQUENCE LISTING

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 2004

<210> 231

<211> 1397

<212> DNA

<213> Rat

<400> 231

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 480
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 720
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 780
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 840
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 900
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1011c2PCTSEQUENCE LISTING

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 1080
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 1200
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 1397

<210> 232

<211> 861

<212> DNA

<213> Rat

<400> 232

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 420
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 480
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 720
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 780
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 840
 ttcttgaagt catcgaacct a
 861

1011c2PCTSEQUENCE LISTING

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 <211> 445
 <212> DNA
 <213> Mouse

<400> 233
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 180
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 240
 cggccgtatt cccagcccat ctcttactca ctagaagttc ctggaagagt catttatcct
 300
 cttacctgat gccctttctc ctcaatcaga gtggatccct tctctactac ttgactttgg
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 445

<210> 234
 <211> 565
 <212> DNA
 <213> Human

<400> 234
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 tctcgtgggt tctgtctacc tggcctggat cctgttcttc gtgctctatg atttctgcat
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 240
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 420
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 540
 tagatcaatc aaaaaaaaaa aaaaa
 565

<210> 235
 <211> 476
 <212> DNA
 <213> Human

1011c2PCTSEQUENCE LISTING

<400> 235

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 240
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 476

<210> 236

<211> 607

<212> DNA

<213> Human

<400> 236

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 420
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 607

<210> 237

<211> 513

<212> DNA

<213> Mouse

<400> 237

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1011c2PCTSEQUENCE LISTING

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 360
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 513

<210> 238

<211> 944

<212> DNA

<213> Rat

<400> 238

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 180
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 420
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 480
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 gcaaagagaa agaaaagcct tcctacgaca ctgaggcaga tcctagttag ggattaatga
 720
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 840
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 944

1011c2PCTSEQUENCE LISTING

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 <211> 386
 <212> DNA
 <213> Rat

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 180
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 gccagattt cttctaccga tgcttc
 386

<210> 240
 <211> 228
 <212> DNA
 <213> Rat

<400> 240
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 120
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 180
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 228

<210> 241
 <211> 452
 <212> DNA
 <213> Human

<400> 241
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 180
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 240
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 300
 tctgagttag ctaactgaca caatgaaact gtcaggcatg tttctgctcc tctctctggc
 360

1011c2PCTSEQUENCE LISTING

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 420
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 452

<210> 242
 <211> 1311
 <212> DNA
 <213> Mouse

<400> 242
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 180
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 720
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1011c2PCTSEQUENCE LISTING

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 <211> 399
 <212> DNA
 <213> Mouse

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 <211> 1421
 <212> DNA
 <213> Mouse

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 <222> (1370) ... (1370)
 <221> unsure
 <222> (1395) ... (1395)

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 120
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 300
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 420
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1011c2PCTSEQUENCE LISTING

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 1421

<210> 245
 <211> 461
 <212> DNA
 <213> Mouse

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 461

<210> 246
 <211> 1280
 <212> DNA

1011c2PCTSEQUENCE LISTING

<213> Mouse

<400> 246

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 720
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<213> Rat

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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<400> 255

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 <212> DNA
 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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<211> 946
<212> DNA
<213> Mouse

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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<211> 1335
<212> DNA
<213> Mouse

<400> 261
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1011c2PCTSEQUENCE LISTING

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<213> Mouse

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1011c2PCTSEQUENCE LISTING

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 <211> 764
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 <213> Mouse

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<210> 264
 <211> 1697
 <212> DNA
 <213> Mouse

1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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 <213> Mouse

<220>

<400> 265
 gttttcttct ccaggctgaa gacctgaacg tcaagttgga aggggagcct tccatgcgga
 60
 aaccaaagca gcggccgcgg ccggagcccc tcatcatccc caccaaggcg ggcactttca
 120
 tcgcccctcc tgtctactcc aacatcaccc cttaccaga
 159

<210> 266
 <211> 292
 <212> DNA
 <213> Mouse

<400> 266
 gtgggggtccc agacttgcca accaaagggc cattcctggt atatggttct ggcttcagct
 60
 ctggtggcat ggactatggt atggttggtg gcaaggagcg tgggaccgag tctcgcttca
 120
 aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc
 180
 acaaaaacgg cgctatagtg gcccctggta agaccgaggg aggttcacca tacaaccagt
 240
 ttgatataat ccaggtgac aactgggtg gccatacggg tcctgctggt ga
 292

<210> 267
 <211> 339
 <212> DNA
 <213> Mouse

<400> 267
 ccactgacct tcccagaagg tgacagccgg cggcggatgt tgtcaaggag ccgagatagt
 60
 ccagcagtc ctcggtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg
 120
 atgagaagtc accacagtga tctcacattt tgcgagatta tcctgatgga gatggagtcc
 180
 catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataccga
 240
 cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg
 300

1011c2PCTSEQUENCE LISTING

tacactagct cagaagagtt tgcagctgat gctctgctg
339

<210> 268
<211> 153
<212> DNA
<213> Mouse

<400> 268
ctgaagttct ctcaccccttg tctggaagac cataatagtt actgcattaa tggagcatgt
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gcattccacc atgagctgaa gcaagccatt tgcagatgct ttactgggta tacgggacaa
120
cgatgtgagc atttgaccct aacttcgtat gct
153

<210> 269
<211> 153
<212> DNA
<213> Human

<400> 269
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60
gcattccacc atgagctaga gaaagccatc tgcaggtggt ttactgggta tactggagaa
120
agggtgtgagc acttgacttt aacttcatat gct
153

<210> 270
<211> 288
<212> DNA
<213> Human

<400> 270
gcggccgcgc tgctcctgct gctgctggcg ctgtacaccg cgcgtgtgga cgggtccaaa
60
tgcaagtgct cccggaaggg acccaagatc cgctacagcg acgtgaagaa gctggaaatg
120
aagccaaagt acccgcaactg cgaggagaag atggttatca tcaccaccaa gagcgtgtcc
180
aggtagcgag gtcaggagca ctgcctgcac cccaagctgc agagcaccaa gcgcttcac
240
aagtgggtaca acgcctggaa cgagaagcgc aggtctacg aagaatag
288

<210> 271
<211> 234
<212> DNA
<213> Mouse

<400> 271
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60
gaaatgaagc caaagtaccc aactgcgag gagaagatgg ttatcgtcac caccaagagc

1011c2PCTSEQUENCE LISTING

120
 atgtccaggt accggggcca ggagcactgc ctgcacccta agctgcagag caccaaagcg
 180
 ttcataaagt ggtacaatgc ctggaacgag aagcgcaggg tctacgaaga atag
 234

<210> 272
 <211> 234
 <212> DNA
 <213> Human
 <400> 272

tccaaatgca agtgctcccc gaagggaccc aagatccgct acagcgacgt gaagaagctg
 60
 gaaatgaagc caaagtaccc gcactgagag gagaagatgg ttatcatcac caccaagagc
 120
 gtgtccaggt accgaggtca ggagcactgc ctgcacccca agctgcagag caccaagcgc
 180
 ttcataaagt ggtacaacgc ctggaacgag aagcgcaggg tctacgaaga atag
 234

<210> 273
 <211> 645
 <212> DNA
 <213> Mouse

<400> 273
 atgtgtgcgc tccgctcctt gcttccacac ctgggactgt tctgtgcct ggctctgcac
 60
 ttatccccct ccctctctgc cagtgataat gggctctgag tggctcctga taacatctac
 120
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 180
 acagtgcagg tccccgtgaa cgattcagtc agtgccgtga tctgaaagc agtgaaggag
 240
 gacgacagcc cagtgggcac ctggagtggg acatatgaga agtgcaacga cagcagtgtc
 300
 tactataact tgacatccca aagccagtcg gtcttccaga caaactggac agttcctact
 360
 tccgaggatg tgactaaagt caacctgcag gtcctcatcg tcgtcaatcg cacagcctca
 420
 aagtcacccg tgaaaatgga acaagtacaa ccctcagcct caaccctat tctgagagt
 480
 tctgagacca gccagaccat aaacacgact ccaactgtga acacagccaa gactacagcc
 540
 aaggacacag ccaacaccac agccgtgacc acagccaata ccacagccaa taccacagcc
 600
 gtgaccacag ccaagaccac agccaaaagc ctggccatcc gcact
 645

<210> 274
 <211> 63
 <212> DNA
 <213> Mouse

<400> 274

1011c2PCTSEQUENCE LISTING

gggtacagtg atggttacca agtgtgtagt aggttcggaa gcaaagtgcc tcagtttctg

60

aac

63

<210> 275
 <211> 388
 <212> PRT
 <213> Mouse
 <400> 275

Met	Gly	Leu	Glu	Pro	Ser	Trp	Tyr	Leu	Leu	Leu	Cys	Leu	Ala	Val	Ser
1				5				10						15	
Gly	Ala	Ala	Gly	Thr	Asp	Pro	Pro	Thr	Ala	Pro	Thr	Thr	Ala	Glu	Arg
			20					25					30		
Gln	Arg	Gln	Pro	Thr	Asp	Ile	Ile	Leu	Asp	Cys	Phe	Leu	Val	Thr	Glu
		35				40					45				
Asp	Arg	His	Arg	Gly	Ala	Phe	Ala	Ser	Ser	Gly	Asp	Arg	Glu	Arg	Ala
	50				55					60					
Leu	Leu	Val	Leu	Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu
65				70					75					80	
Gly	Ile	Thr	Asp	Phe	Gln	Gly	Ser	Thr	Glu	Thr	Lys	Gln	Asp	Ser	Pro
			85					90					95		
Val	Ile	Phe	Glu	Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu
			100					105					110		
Ala	Leu	Leu	His	Ala	Asp	Cys	Ser	Gly	Lys	Ala	Val	Thr	Cys	Glu	Ile
		115					120					125			
Ser	Lys	Tyr	Phe	Leu	Gln	Ala	Arg	Gln	Glu	Ala	Thr	Phe	Glu	Lys	Ala
	130				135						140				
His	Trp	Phe	Ile	Ser	Asn	Met	Gln	Val	Ser	Arg	Gly	Gly	Pro	Ser	Val
145				150					155					160	
Ser	Met	Val	Met	Lys	Thr	Leu	Arg	Asp	Ala	Glu	Val	Gly	Ala	Val	Arg
			165						170					175	
His	Pro	Thr	Leu	Asn	Leu	Pro	Leu	Ser	Ala	Gln	Gly	Thr	Val	Lys	Thr
			180					185					190		
Gln	Val	Glu	Phe	Gln	Val	Thr	Ser	Glu	Thr	Gln	Thr	Leu	Asn	His	Leu
		195					200					205			
Leu	Gly	Ser	Ser	Val	Ser	Leu	His	Cys	Ser	Phe	Ser	Met	Ala	Pro	Asp
	210				215					220					
Leu	Asp	Leu	Thr	Gly	Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Ser	Gly
225				230					235					240	
Gln	Leu	Val	Tyr	Ser	Trp	Lys	Thr	Gly	Gln	Gly	Gln	Ala	Lys	Arg	Lys
			245						250					255	
Gly	Ala	Thr	Leu	Glu	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Gly	Asn	Ala	Ser
			260					265					270		
Leu	Thr	Leu	Pro	Asn	Leu	Thr	Leu	Lys	Asp	Glu	Gly	Thr	Tyr	Ile	Cys
		275					280					285			
Gln	Ile	Ser	Thr	Ser	Leu	Tyr	Gln	Ala	Gln	Gln	Ile	Met	Pro	Leu	Asn
	290				295						300				
Ile	Leu	Ala	Pro	Pro	Lys	Val	Gln	Leu	His	Leu	Ala	Asn	Lys	Asp	Pro
305					310					315				320	
Leu	Pro	Ser	Leu	Val	Cys	Ser	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val
			325						330					335	
Gly	Val	Thr	Trp	Ile	Arg	Glu	Glu	Leu	Gly	Gly	Ile	Pro	Ala	Gln	Val
			340					345					350		
Ser	Gly	Ala	Ser	Phe	Ser	Ser	Leu	Arg	Gln	Ser	Thr	Met	Gly	Thr	Tyr

1011c2PCTSEQUENCE LISTING

	355		360		365
Ser	Ile	Ser	Ser	Thr	Val
	370				375
Tyr	Thr	Cys	Gln		
385					380

<210> 276
 <211> 151
 <212> PRT
 <213> Rat

<400> 276

Met	Ala	Glu	Pro	Trp	Ala	Gly	Gln	Phe	Leu	Gln	Ala	Leu	Pro	Ala	Thr
1				5					10					15	
Val	Leu	Gly	Ala	Leu	Gly	Thr	Leu	Gly	Ser	Glu	Phe	Leu	Arg	Glu	Trp
			20					25					30		
Glu	Thr	Gln	Asp	Met	Arg	Val	Thr	Leu	Phe	Lys	Leu	Leu	Leu	Leu	Trp
		35					40					45			
Leu	Val	Leu	Ser	Leu	Leu	Gly	Ile	Gln	Leu	Ala	Trp	Gly	Phe	Tyr	Gly
	50					55					60				
Asn	Thr	Val	Thr	Gly	Leu	Tyr	His	Arg	Pro	Gly	Lys	Trp	Gln	Gln	Met
65					70					75					80
Lys	Leu	Ser	Lys	Leu	Thr	Glu	Asn	Lys	Gly	Arg	Gln	Gln	Glu	Lys	Gly
			85						90					95	
Leu	Gln	Arg	Tyr	Arg	Trp	Val	Cys	Trp	Leu	Leu	Cys	Cys	Thr	Leu	Leu
			100					105					110		
Leu	Ser	Arg	Pro	Leu	Arg	Gln	Leu	Gln	Arg	Ala	Trp	Val	Gly	Gly	Leu
		115					120					125			
Glu	Tyr	His	Asp	Ala	Pro	Arg	Val	Ser	Leu	His	Cys	Pro	Gln	Pro	Cys
	130					135					140				
Leu	Gln	Gln	Arg	Gln	Val	Leu									
145					150										

<210> 277
 <211> 163
 <212> PRT
 <213> Rat

<400> 277

Met	Pro	Leu	Val	Thr	Thr	Leu	Phe	Tyr	Ala	Cys	Phe	Tyr	His	Tyr	Thr
1				5					10					15	
Glu	Ser	Glu	Gly	Thr	Phe	Ser	Ser	Pro	Val	Asn	Leu	Lys	Lys	Thr	Phe
			20					25					30		
Lys	Ile	Pro	Asp	Arg	Gln	Tyr	Val	Leu	Thr	Ala	Leu	Ala	Ala	Arg	Ala
		35					40					45			
Lys	Leu	Arg	Ala	Trp	Asn	Asp	Val	Asp	Ala	Leu	Phe	Thr	Thr	Lys	Asn
	50					55					60				
Trp	Leu	Gly	Tyr	Thr	Lys	Lys	Arg	Ala	Pro	Ile	Gly	Phe	His	Arg	Val
65					70					75					80
Val	Glu	Ile	Leu	His	Lys	Asn	Ser	Ala	Pro	Val	Gln	Ile	Leu	Gln	Glu
				85					90					95	
Tyr	Val	Asn	Leu	Val	Glu	Asp	Val	Asp	Thr	Lys	Leu	Asn	Leu	Ala	Thr
			100					105					110		
Lys	Phe	Lys	Cys	His	Asp	Val	Val	Ile	Asp	Thr	Cys	Arg	Asp	Leu	Lys
		115					120					125			

1011c2PCTSEQUENCE LISTING

Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
 130 135 140
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
 145 150 155 160
 Trp Lys Asn

<210> 278

<211> 330

<212> PRT

<213> Rat

<400> 278

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1 5 10 15
 Ala Leu Trp Leu Leu Leu Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20 25 30
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35 40 45
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50 55 60
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65 70 75 80
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85 90 95
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100 105 110
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115 120 125
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
 130 135 140
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145 150 155 160
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165 170 175
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180 185 190
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195 200 205
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210 215 220
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225 230 235 240
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245 250 255
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260 265 270
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275 280 285
 Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290 295 300
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305 310 315 320
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325 330

1011c2PCTSEQUENCE LISTING

<210> 279

<211> 61

<212> PRT

<213> Rat

<400> 279

Met	Glu	Asn	Ile	Tyr	Tyr	Thr	Asn	Leu	Ile	Thr	Ile	Leu	Gly	Asn	Lys
1				5					10					15	
His	Ala	Asn	Gln	Met	Glu	Leu	Asn	Leu	Gln	Ala	Leu	Ile	Leu	Ser	Pro
		20					25						30		
Trp	Phe	Ala	Val	Cys	Ala	Pro	Pro	Gly	Phe	Ala	Arg	Asp	Gln	Ala	Val
		35					40					45			
Arg	Gly	Leu	Ala	Leu	Ala	Gly	Arg	Arg	Ile	Thr	Val	Val			
	50					55					60				

<210> 280

<211> 105

<212> PRT

<213> Rat

<400> 280

Met	Leu	Arg	Arg	Gln	Leu	Val	Trp	Trp	His	Leu	Leu	Ala	Leu	Leu	Phe
1				5					10					15	
Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Ser	Pro	Gln	Ala
			20					25					30		
Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly	Asp	Tyr	Gly
		35					40					45			
Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ile
	50					55					60				
Pro	Gly	Asn	His	Gly	Asn	Asn	Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu
65					70					75					80
Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly
			85						90					95	
Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly							
			100					105							

<210> 281

<211> 27

<212> PRT

<213> Mouse

<400> 281

Met	Leu	Lys	Ala	Ser	Leu	His	Ile	Leu	Phe	Leu	Gly	Ile	Leu	Asn	Val
1				5					10					15	
Pro	Ile	Val	Asp	Thr	Ser	Thr	Lys	Thr	Gly	Val					
			20					25							

<210> 282

<211> 169

<212> PRT

<213> Mouse

<400> 282

Met	Ser	Gly	Leu	Arg	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Leu	Val	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1011c2PCTSEQUENCE LISTING

1				5				10				15					
Ser	Arg	Leu	Pro	Arg	Val	Ile	Ser	Gln	Gln	Ser	Val	Cys	Arg	Ala	Arg		
			20					25					30				
Pro	Ile	Trp	Trp	Gly	Thr	Gln	Arg	Arg	Gly	Ser	Glu	Thr	Met	Ala	Gly		
		35					40					45					
Ala	Ala	Val	Lys	Tyr	Leu	Ser	Gln	Glu	Glu	Ala	Gln	Ala	Val	Asp	Gln		
		50				55					60						
Glu	Leu	Phe	Asn	Glu	Tyr	Gln	Phe	Ser	Val	Asp	Gln	Leu	Met	Glu	Leu		
65				70						75				80			
Ala	Gly	Leu	Ser	Cys	Ala	Thr	Ala	Ile	Ala	Lys	Ala	Tyr	Pro	Pro	Thr		
				85					90				95				
Ser	Met	Ser	Lys	Ser	Pro	Pro	Thr	Val	Leu	Val	Ile	Cys	Gly	Pro	Gly		
			100					105					110				
Asn	Asn	Gly	Gly	Asp	Gly	Leu	Val	Cys	Ala	Arg	His	Leu	Lys	Leu	Phe		
		115					120					125					
Gly	Tyr	Gln	Pro	Thr	Ile	Tyr	Tyr	Pro	Lys	Arg	Pro	Asn	Lys	Pro	Leu		
	130					135					140						
Phe	Thr	Gly	Leu	Val	Thr	Gln	Cys	Gln	Lys	Met	Asp	Ile	Pro	Phe	Leu		
145					150					155					160		
Gly	Glu	Met	Pro	Pro	Glu	Asp	Gly	Met									
				165													

<210> 283
 <211> 61
 <212> PRT
 <213> Mouse

Met	Glu	Lys	Gln	Met	Asp	Ala	Ser	Val	Ser	Val	Ile	Phe	Gly	Ser	Ile		
1				5					10					15			
Val	Ile	Ser	Ala	Phe	Leu	Tyr	Leu	Ser	Leu	Ala	Gly	Pro	Trp	Ala	Val		
			20					25					30				
Thr	Val	Thr	Gln	Met	Arg	Thr	Ile	Ile	Ile	Thr	Met	Asp	Gln	Leu	Arg		
		35				40						45					
Asp	Ala	Leu	Ile	Leu	Asp	Gln	Leu	Lys	Val	Ala	Val	Ser					
	50					55					60						

<210> 284
 <211> 131
 <212> PRT
 <213> Mouse

Met	Ala	Pro	Ser	Leu	Trp	Lys	Gly	Leu	Val	Gly	Val	Gly	Leu	Phe	Ala		
1				5				10					15				
Leu	Ala	His	Ala	Ala	Phe	Ser	Ala	Ala	Gln	His	Arg	Ser	Tyr	Met	Arg		
			20					25					30				
Leu	Thr	Glu	Lys	Glu	Asp	Glu	Ser	Leu	Pro	Ile	Asp	Ile	Val	Leu	Gln		
		35				40					45						
Thr	Leu	Leu	Ala	Phe	Ala	Val	Thr	Cys	Tyr	Gly	Ile	Val	His	Ile	Ala		
	50					55					60						
Gly	Glu	Phe	Lys	Asp	Met	Asp	Ala	Thr	Ser	Glu	Leu	Lys	Asn	Lys	Thr		
65				70						75				80			
Phe	Asp	Thr	Leu	Arg	Asn	His	Pro	Ser	Phe	Tyr	Val	Phe	Asn	His	Arg		
				85					90					95			

1011c2PCTSEQUENCE LISTING

Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
 100 105 110
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
 115 120 125
 Leu Arg Arg
 130

<210> 285
 <211> 78
 <212> PRT
 <213> Mouse

<400> 285
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
 1 5 10 15
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
 20 25 30
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
 35 40 45
 Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
 50 55 60
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
 65 70 75

<210> 286
 <211> 206
 <212> PRT
 <213> Mouse

<400> 286
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
 1 5 10 15
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
 20 25 30
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
 35 40 45
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
 50 55 60
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
 65 70 75 80
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
 85 90 95
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
 100 105 110
 Trp Ile Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
 115 120 125
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
 130 135 140
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
 145 150 155 160
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
 165 170 175
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
 180 185 190
 Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser

1011c2PCTSEQUENCE LISTING

195

200

205

<210> 287
 <211> 169
 <212> PRT
 <213> Mouse

<400> 287

Met	Ser	Gly	Leu	Arg	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Leu	Val	Ala	Gly
1				5					10					15	
Ser	Arg	Leu	Pro	Arg	Val	Ile	Ser	Gln	Gln	Ser	Val	Cys	Arg	Ala	Arg
			20					25					30		
Pro	Ile	Trp	Trp	Gly	Thr	Gln	Arg	Arg	Gly	Ser	Glu	Thr	Met	Ala	Gly
		35				40					45				
Ala	Ala	Val	Lys	Tyr	Leu	Ser	Gln	Glu	Glu	Ala	Gln	Ala	Val	Asp	Gln
	50					55					60				
Glu	Leu	Phe	Asn	Glu	Tyr	Gln	Phe	Ser	Val	Asp	Gln	Leu	Met	Glu	Leu
65				70						75				80	
Ala	Gly	Leu	Ser	Cys	Ala	Thr	Ala	Ile	Ala	Lys	Ala	Tyr	Pro	Pro	Thr
				85					90					95	
Ser	Met	Ser	Lys	Ser	Pro	Pro	Thr	Val	Leu	Val	Ile	Cys	Gly	Pro	Gly
			100					105					110		
Asn	Asn	Gly	Gly	Asp	Gly	Leu	Val	Cys	Ala	Arg	His	Leu	Lys	Leu	Phe
		115				120						125			
Gly	Tyr	Gln	Pro	Thr	Ile	Tyr	Tyr	Pro	Lys	Arg	Pro	Asn	Lys	Pro	Leu
	130					135					140				
Phe	Thr	Gly	Leu	Val	Thr	Gln	Cys	Gln	Lys	Met	Asp	Ile	Pro	Phe	Leu
145					150					155					160
Gly	Glu	Met	Pro	Pro	Glu	Asp	Gly	Met							
				165											

<210> 288
 <211> 114
 <212> PRT
 <213> Mouse

<400> 288

Met	Ser	Val	Thr	Ile	Gly	Arg	Leu	Ala	Leu	Phe	Leu	Ile	Gly	Ile	Leu
1				5					10					15	
Leu	Cys	Pro	Val	Ala	Pro	Ser	Leu	Thr	Arg	Ser	Trp	Pro	Gly	Pro	Asp
			20					25					30		
Thr	Cys	Ser	Leu	Phe	Leu	Gln	His	Ser	Leu	Ser	Leu	Ser	Leu	Arg	Leu
		35				40					45				
Gly	Gln	Ser	Leu	Glu	Gly	Gly	Leu	Ser	Val	Cys	Phe	His	Val	Cys	Ile
	50					55					60				
His	Ala	Cys	Glu	Cys	Val	Ala	Cys	Cys	Arg	Val	Leu	Trp	Asp	Pro	Lys
65				70						75				80	
Pro	Arg	Gly	Ser	Ser	Leu	Cys	Arg	Trp	Val	Leu	Gly	Ser	Ile	Thr	Cys
				85					90					95	
Leu	Phe	Met	Tyr	Glu	Val	Gly	Gly	Trp	Thr	Gln	Gly	Gly	Leu	Ile	Val
			100					105					110		
Ser	Leu														

<210> 289

1011c2PCTSEQUENCE LISTING

<211> 46
 <212> PRT
 <213> Mouse

<400> 289
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
 1 5 10 15
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
 20 25 30
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
 35 40 45

<210> 290
 <211> 199
 <212> PRT
 <213> Mouse

<400> 290
 Met Val Leu Pro Thr Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
 1 5 10 15
 Leu Gly Gly Glu Thr Arg Pro Arg Ala Ala Thr Glu Arg Arg Ser Val
 20 25 30
 Gly Pro Ser Ala Arg Arg Gly Ala Gly Pro Arg Val Ser Gly Leu Leu
 35 40 45
 Gly Phe Cys Gln Leu Ser Gln Leu Ala Ser Ala Asp Pro Glu Arg Arg
 50 55 60
 Ser Pro Arg Ala Ile Val Pro Arg Ala Pro Arg Pro Arg Ser Arg Arg
 65 70 75 80
 Arg Pro Cys Leu Pro Gly Phe Ser Arg Arg Phe Pro Arg Glu Arg Arg
 85 90 95
 Ser Pro Gly Gln Pro Pro Ser Arg Thr Pro Gln Pro Pro Gln Pro Cys
 100 105 110
 Arg Gly Pro Ser Pro Gly Thr Ala Gln Thr Arg Ser Asn Leu Arg Gly
 115 120 125
 Trp Gln Arg Gly Gly Ser Ile Val Leu Gln Ala Ser Glu Arg Thr Arg
 130 135 140
 Ala Gly Cys Arg Thr Pro Val Cys Val Ser His Pro Ser Ala Phe Pro
 145 150 155 160
 Pro Pro Arg Ala Leu Phe Gly Val Phe Val Ala Ser Ala Pro Glu Val
 165 170 175
 Val Cys Val Cys Val Ser Val Val Leu Ser Val Cys Leu Leu Ser Pro
 180 185 190
 Arg Gly Lys Thr Leu Val Asp
 195

<210> 291
 <211> 568
 <212> PRT
 <213> Rat

<400> 291
 Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30

1011c2PCTSEQUENCE LISTING

Gln	Ile	Arg	Asp	Lys	Ala	Leu	Phe	His	Asp	Ser	Ser	Val	Ile	Pro	Asp	
		35					40					45				
Gly	Ala	Glu	Ile	Ser	Ser	Tyr	Leu	Phe	Arg	Asp	Thr	Pro	Arg	Arg	Tyr	
	50					55					60					
Phe	Phe	Met	Val	Glu	Glu	Asp	Asn	Thr	Pro	Leu	Ser	Val	Thr	Val	Thr	
65					70					75					80	
Pro	Cys	Asp	Ala	Pro	Leu	Glu	Trp	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Pro	
				85					90					95		
Glu	Glu	Ser	Ser	Ala	Asp	Gly	Ser	Gly	Asp	Pro	Glu	Pro	Leu	Asp	Gln	
			100					105					110			
Gln	Lys	Gln	Gln	Met	Thr	Asp	Val	Glu	Gly	Thr	Glu	Leu	Phe	Ser	Tyr	
		115					120					125				
Lys	Gly	Asn	Asp	Val	Glu	Tyr	Phe	Leu	Ser	Ser	Ser	Ser	Pro	Ser	Gly	
	130					135					140					
Leu	Tyr	Gln	Leu	Glu	Leu	Leu	Ser	Thr	Glu	Lys	Asp	Thr	His	Phe	Lys	
145					150					155					160	
Val	Tyr	Ala	Thr	Thr	Thr	Pro	Glu	Ser	Asp	Gln	Pro	Tyr	Pro	Asp	Leu	
				165					170					175		
Pro	Tyr	Asp	Pro	Arg	Val	Asp	Val	Thr	Ser	Ile	Gly	Arg	Thr	Thr	Val	
			180					185					190			
Thr	Leu	Ala	Trp	Lys	Gln	Ser	Pro	Thr	Ala	Ser	Met	Leu	Lys	Gln	Pro	
		195					200					205				
Ile	Glu	Tyr	Cys	Val	Val	Ile	Asn	Lys	Glu	His	Asn	Phe	Lys	Ser	Leu	
	210					215					220					
Cys	Ala	Ala	Glu	Thr	Lys	Met	Ser	Ala	Asp	Asp	Ala	Phe	Met	Val	Ala	
225					230					235					240	
Pro	Lys	Pro	Gly	Leu	Asp	Phe	Ser	Pro	Phe	Asp	Phe	Ala	His	Phe	Gly	
				245					250					255		
Phe	Pro	Thr	Asp	Asn	Leu	Gly	Lys	Asp	Arg	Ser	Phe	Leu	Ala	Lys	Pro	
			260					265					270			
Ser	Pro	Lys	Val	Gly	Arg	His	Val	Tyr	Trp	Arg	Pro	Lys	Val	Asp	Ile	
		275					280					285				
Lys	Lys	Ile	Cys	Ile	Gly	Ser	Lys	Asn	Ile	Phe	Thr	Val	Ser	Asp	Leu	
	290				295						300					
Lys	Pro	Asn	Thr	Gln	Tyr	Tyr	Phe	Asp	Val	Phe	Met	Val	Asn	Thr	Asn	
305					310					315					320	
Thr	Asn	Met	Asn	Thr	Ala	Phe	Val	Gly	Ala	Phe	Ala	Arg	Thr	Lys	Glu	
				325					330					335		
Glu	Ala	Lys	Gln	Lys	Thr	Val	Glu	Leu	Lys	Asp	Gly	Arg	Val	Thr	Asp	
			340					345					350			
Val	Val	Val	Lys	Arg	Lys	Gly	Lys	Lys	Phe	Leu	Arg	Phe	Ala	Pro	Val	
		355					360					365				
Ser	Ser	His	Gln	Lys	Val	Thr	Leu	Phe	Ile	His	Ser	Cys	Met	Asp	Thr	
	370					375					380					
Val	Gln	Val	Gln	Val	Arg	Arg	Asp	Gly	Lys	Leu	Leu	Leu	Ser	Gln	Asn	
385					390					395					400	
Val	Glu	Gly	Ile	Arg	Gln	Phe	Gln	Leu	Arg	Gly	Lys	Pro	Lys	Gly	Lys	
				405					410					415		
Tyr	Leu	Ile	Arg	Leu	Lys	Gly	Asn	Lys	Lys	Gly	Ala	Ser	Met	Leu	Lys	
			420					425					430			
Ile	Leu	Ala	Thr	Thr	Arg	Pro	Ser	Lys	His	Ala	Phe	Pro	Ser	Leu	Pro	
		435						440				445				
Asp	Asp	Thr	Arg	Ile	Lys	Ala	Phe	Asp	Lys	Leu	Arg	Thr	Cys	Ser	Ser	
	450					455					460					
Val	Thr	Val	Ala	Trp	Leu	Gly	Thr	Gln	Glu	Arg	Arg	Lys	Phe	Cys	Ile	

1011c2PCTSEQUENCE LISTING

465 470 475 480
 Tyr Arg Lys Glu Val Gly Gly Asn Tyr Ser Glu Glu Gln Lys Arg Arg
 485 490 495
 Glu Arg Asn Gln Cys Leu Gly Pro Asp Thr Arg Lys Lys Ser Glu Lys
 500 505 510
 Val Leu Cys Lys Tyr Phe His Ser Gln Asn Leu Gln Lys Ala Val Thr
 515 520 525
 Thr Glu Thr Ile Arg Asp Leu Gln Pro Gly Lys Ser Tyr Leu Leu Asp
 530 535 540
 Val Tyr Val Val Gly His Gly Gly His Ser Val Lys Tyr Gln Ser Lys
 545 550 555 560
 Leu Val Lys Thr Arg Lys Val Cys
 565

<210> 292
 <211> 123
 <212> PRT
 <213> Mouse

<400> 292
 Met Leu Thr Glu Pro Ala Gln Leu Phe Val His Lys Lys Asn Gln Pro
 1 5 10 15
 Pro Ser His Ser Ser Leu Arg Leu His Phe Arg Thr Leu Ala Gly Ala
 20 25 30
 Leu Ala Leu Ser Ser Thr Gln Met Ser Trp Gly Leu Gln Ile Leu Pro
 35 40 45
 Cys Leu Ser Leu Ile Leu Leu Leu Trp Asn Gln Val Pro Gly Leu Glu
 50 55 60
 Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu
 65 70 75 80
 Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr
 85 90 95
 Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg
 100 105 110
 Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser
 115 120

<210> 293
 <211> 66
 <212> PRT
 <213> Mouse

<400> 293
 Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu
 1 5 10 15
 Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys
 20 25 30
 Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr
 35 40 45
 His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala
 50 55 60
 Leu Cys
 65

<210> 294

1011c2PCTSEQUENCE LISTING

<211> 294

<212> PRT

<213> Rat

<400> 294

Met	Thr	Val	Phe	Arg	Lys	Val	Thr	Thr	Met	Ile	Ser	Trp	Met	Leu	Leu
1				5					10					15	
Ala	Cys	Ala	Leu	Pro	Cys	Ala	Ala	Asp	Pro	Met	Leu	Gly	Ala	Phe	Ala
			20					25					30		
Arg	Arg	Asp	Phe	Gln	Lys	Gly	Gly	Pro	Gln	Leu	Val	Cys	Ser	Leu	Pro
		35					40					45			
Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Ser	Ser	Gly
	50					55					60				
Met	Val	Gly	Arg	Met	Gly	Phe	Pro	Gly	Lys	Asp	Gly	Gln	Asp	Gly	Gln
65					70					75					80
Asp	Gly	Asp	Arg	Gly	Asp	Ser	Gly	Glu	Glu	Gly	Pro	Pro	Gly	Arg	Thr
			85					90						95	
Gly	Asn	Arg	Gly	Lys	Gln	Gly	Pro	Lys	Gly	Lys	Ala	Gly	Ala	Ile	Gly
			100					105					110		
Arg	Ala	Gly	Pro	Arg	Gly	Pro	Lys	Gly	Val	Ser	Gly	Thr	Pro	Gly	Lys
		115					120					125			
His	Gly	Ile	Pro	Gly	Lys	Lys	Gly	Pro	Lys	Gly	Lys	Lys	Gly	Glu	Pro
	130					135					140				
Gly	Leu	Pro	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Ser	Arg	Ala	Lys	Ser	Ala
145					150					155					160
Phe	Ser	Val	Ala	Val	Thr	Lys	Ser	Tyr	Pro	Arg	Glu	Arg	Leu	Pro	Ile
				165					170					175	
Lys	Phe	Asp	Lys	Ile	Leu	Met	Asn	Glu	Gly	Gly	His	Tyr	Asn	Ala	Ser
			180					185					190		
Ser	Gly	Lys	Phe	Val	Cys	Ser	Val	Pro	Gly	Ile	Tyr	Tyr	Phe	Thr	Tyr
		195					200					205			
Asp	Ile	Thr	Leu	Ala	Asn	Lys	His	Leu	Ala	Ile	Gly	Leu	Val	His	Asn
	210				215						220				
Gly	Gln	Tyr	Arg	Ile	Arg	Thr	Phe	Asp	Ala	Asn	Thr	Gly	Asn	His	Asp
225					230					235					240
Val	Ala	Ser	Gly	Ser	Thr	Ile	Leu	Ala	Leu	Lys	Glu	Gly	Asp	Glu	Val
				245					250					255	
Trp	Leu	Gln	Ile	Phe	Tyr	Ser	Glu	Gln	Asn	Gly	Leu	Phe	Tyr	Asp	Pro
			260					265					270		
Tyr	Trp	Thr	Asp	Ser	Leu	Phe	Thr	Gly	Phe	Leu	Ile	Tyr	Ala	Asp	Gln
		275					280					285			
Gly	Asp	Pro	Asn	Glu	Val										
	290														

<210> 295

<211> 243

<212> PRT

<213> Rat

<400> 295

Met	Arg	Pro	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ser	Gly	Ser
1				5					10					15	
Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	Gln	Pro
			20					25					30		
Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	Leu	Pro	Gly

1011c2PCTSEQUENCE LISTING

35	40	45
Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu		
50	55	60
Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro		
65	70	75
Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly		
85	90	95
Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu		
100	105	110
Ser Arg Val Pro Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val		
115	120	125
Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr		
130	135	140
Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr		
145	150	155
Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala		
165	170	175
Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser		
180	185	190
Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln		
195	200	205
Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp		
210	215	220
Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro		
225	230	235
Val Phe Ala		240

<210> 296

<211> 444

<212> PRT

<213> Rat

<400> 296

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly		
1	5	10
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser		
20	25	30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu		
35	40	45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr		
50	55	60
Pro Glu Glu Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val		
65	70	75
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile		
85	90	95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr		
100	105	110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn		
115	120	125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg		
130	135	140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu		
145	150	155
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser		

1011c2PCTSEQUENCE LISTING

				165					170					175			
Asp	Tyr	Ile	Phe	Leu	Thr	Thr	Val	Leu	Ser	Thr	Pro	Gln	Arg	Asn	Phe		
			180					185					190				
Glu	Ile	Ala	Phe	Lys	Met	Phe	Asp	Leu	Asn	Gly	Asp	Gly	Glu	Val	Asp		
		195					200					205					
Met	Glu	Glu	Phe	Glu	Gln	Val	Gln	Ser	Ile	Ile	Arg	Ser	Gln	Thr	Ser		
	210				215						220						
Met	Gly	Met	Arg	His	Arg	Asp	Arg	Pro	Thr	Thr	Gly	Asn	Thr	Leu	Lys		
225					230						235				240		
Ser	Gly	Leu	Cys	Ser	Ala	Leu	Thr	Thr	Tyr	Phe	Phe	Gly	Ala	Asp	Leu		
			245						250					255			
Lys	Gly	Lys	Leu	Thr	Ile	Lys	Asn	Phe	Leu	Glu	Phe	Gln	Arg	Lys	Leu		
			260					265					270				
Gln	His	Asp	Val	Leu	Lys	Leu	Glu	Phe	Glu	Arg	His	Asp	Pro	Val	Asp		
		275					280					285					
Gly	Arg	Ile	Ser	Glu	Arg	Gln	Phe	Gly	Gly	Met	Leu	Leu	Ala	Tyr	Ser		
	290					295					300						
Gly	Val	Gln	Ser	Lys	Lys	Leu	Thr	Ala	Met	Gln	Arg	Gln	Leu	Lys	Lys		
305					310					315					320		
His	Phe	Lys	Asp	Gly	Lys	Gly	Leu	Thr	Phe	Gln	Glu	Val	Glu	Asn	Phe		
			325						330					335			
Phe	Thr	Phe	Leu	Lys	Asn	Ile	Asn	Asp	Val	Asp	Thr	Ala	Leu	Ser	Phe		
			340					345					350				
Tyr	His	Met	Ala	Gly	Ala	Ser	Leu	Asp	Lys	Val	Thr	Met	Gln	Gln	Val		
		355					360					365					
Ala	Arg	Thr	Val	Ala	Lys	Val	Glu	Leu	Ser	Asp	His	Val	Cys	Asp	Val		
	370					375					380						
Val	Phe	Ala	Leu	Phe	Asp	Cys	Asp	Gly	Asn	Gly	Glu	Leu	Ser	Asn	Lys		
385					390					395					400		
Glu	Phe	Val	Ser	Ile	Met	Lys	Gln	Arg	Leu	Met	Arg	Gly	Leu	Glu	Lys		
			405						410					415			
Pro	Lys	Asp	Met	Gly	Phe	Thr	Arg	Leu	Met	Gln	Ala	Met	Trp	Lys	Cys		
		420						425					430				
Ala	Gln	Glu	Thr	Ala	Trp	Asp	Phe	Ala	Leu	Pro	Lys						
		435					440										

<210> 297
 <211> 65
 <212> PRT
 <213> Human

<400> 297

Met	Thr	Met	Leu	His	Leu	Ala	Val	Ile	Phe	Leu	Phe	Ser	Ala	Leu	Ser		
1				5					10					15			
Arg	Ala	Leu	Val	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser		
			20					25					30				
Trp	Ala	Asp	Tyr	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala		
		35					40					45					
Leu	Asp	Val	Gly	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser		
	50					55					60						
Leu																	
65																	

<210> 298
 <211> 52

1011c2PCTSEQUENCE LISTING

<212> PRT

<213> Human

<400> 298

Met	Lys	Ile	Asn	Ile	Ile	Gln	Gly	Ser	Ile	Met	Ile	Leu	Leu	Ile	Cys
1				5					10					15	
Leu	Ser	Gln	Thr	Cys	Thr	Ser	Leu	Pro	Val	Gln	Glu	Ala	Leu	Ile	Thr
			20					25					30		
Phe	Cys	His	Leu	Tyr	Phe	Thr	Tyr	Cys	Tyr	Ser	Gly	Asn	Ser	Asn	Lys
		35					40					45			
Met	Gln	Val	Leu												
	50														

<210> 299

<211> 41

<212> PRT

<213> Human

<400> 299

Met	Pro	Cys	Val	Leu	Phe	Phe	Phe	Phe	Phe	Leu	Ser	Thr	Ser	Lys	Ser
1				5					10					15	
Met	Ile	Tyr	Ser	Ser	Leu	Met	Leu	Gly	Leu	Tyr	Ile	Pro	Ser	Glu	Ala
			20					25					30		
Cys	Val	Leu	Gly	Leu	Lys	Phe	Lys	Phe							
		35					40								

<210> 300

<211> 80

<212> PRT

<213> Mouse

<400> 300

Met	Val	Trp	Gly	Thr	Leu	Leu	Gly	Arg	Val	Leu	Ala	Ala	Leu	Leu	Asn
1				5					10					15	
Ile	Val	Pro	Thr	Glu	Ser	Ser	Tyr	Arg	Ser	Pro	Ser	Phe	Leu	Ala	Gly
			20					25					30		
Phe	Arg	Phe	Cys	Cys	Ser	Pro	Trp	Ser	Gln	His	Phe	Gly	Cys	Gly	Arg
		35					40					45			
Leu	Thr	Ser	Cys	Leu	Pro	Pro	Cys	Val	Asp	Arg	Val	Val	Lys	Thr	Tyr
	50					55					60				
Ser	Ser	Pro	Pro	Cys	Leu	Ser	Val	Asn	Gly	His	Asp	Val	Thr	Ile	Cys
65					70					75					80

<210> 301

<211> 82

<212> PRT

<213> Mouse

<400> 301

Met	Gly	Ser	Val	Leu	Thr	Ser	Cys	Phe	Cys	Val	Gly	Gly	Ser	Ala	Glu
1				5					10					15	
Ala	Trp	Asn	Trp	Leu	Pro	Ser	Ala	Ser	Ser	Leu	Phe	Pro	Cys	Cys	Ile
			20					25					30		
Ala	Thr	Leu	Leu	Pro	Leu	Leu	Phe	Leu	Leu	Pro	His	Leu	His	Ser	Thr
		35					40					45			

1011c2PCTSEQUENCE LISTING

Leu Ser Arg Val Gln Arg Leu Asn Phe Asn Ile Gly His Leu Gly Val
 50 55 60
 Tyr Leu Tyr Val Asn Asn Asp Ile Arg Ser Arg Val Thr Pro Leu Leu
 65 70 75 80
 Ser Ser

<210> 302

<211> 411

<212> PRT

<213> Rat

<400> 302

Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
 1 5 10 15
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
 20 25 30
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
 35 40 45
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
 50 55 60
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
 65 70 75 80
 Ala Gly Glu Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr
 85 90 95
 Asp Val Ala Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val
 100 105 110
 Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Ile Thr Gly
 115 120 125
 Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Lys Lys His Ala
 130 135 140
 Lys Gly Val Arg Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr
 145 150 155 160
 Asp Asp Phe Arg Ser Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu
 165 170 175
 Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe
 180 185 190
 Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu
 195 200 205
 Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu
 210 215 220
 Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln
 225 230 235 240
 Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu
 245 250 255
 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro
 260 265 270
 Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu
 275 280 285
 Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe
 290 295 300
 Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile
 305 310 315 320
 Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser
 325 330 335

1011c2PCTSEQUENCE LISTING

Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu
 340 345 350
 Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu
 355 360 365
 Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu
 370 375 380
 Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser
 385 390 395 400
 Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln
 405 410

<210> 303
 <211> 617
 <212> PRT
 <213> Mouse

<400> 303
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 1 5 10 15
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
 20 25 30
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 35 40 45
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 50 55 60
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 65 70 75 80
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 85 90 95
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 100 105 110
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 115 120 125
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 130 135 140
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 145 150 155 160
 Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 165 170 175
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
 180 185 190
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
 195 200 205
 Leu Gln Glu Asp Thr Val Arg Lys Lys Cys Pro Phe Gln Ser Trp
 210 215 220
 Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
 225 230 235 240
 Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
 245 250 255
 Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
 260 265 270
 Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
 275 280 285
 Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
 290 295 300

1011c2PCTSEQUENCE LISTING

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Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
305          310          315          320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu
          325          330          335
His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp
          340          345          350
Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser
          355          360          365
Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe
          370          375          380
Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe
385          390          395          400
Ala Trp Lys His Val Leu Cys Pro Asp Asp Ala Pro Tyr Pro Thr Gln
          405          410          415
Leu Leu Leu Arg Ser Leu Gly Ser Gly Arg Thr Arg Pro Val Leu Leu
          420          425          430
Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly Ala Leu
          435          440          445
Ala Glu Leu Leu Arg Thr Ala Leu Gly Gly Gly Arg Asp Val Ile Val
          450          455          460
Asp Leu Trp Glu Gly Thr His Val Ala Arg Ile Gly Pro Leu Pro Trp
465          470          475          480
Leu Trp Ala Ala Arg Glu Arg Val Ala Arg Glu Gln Gly Thr Val Leu
          485          490          495
Leu Leu Trp Asn Cys Ala Gly Pro Ser Thr Ala Cys Ser Gly Asp Pro
          500          505          510
Gln Ala Ala Ser Leu Arg Thr Leu Leu Cys Ala Ala Pro Arg Pro Leu
          515          520          525
Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp Ile Pro Arg
          530          535          540
Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp Leu Pro Arg
545          550          555          560
Leu Leu Arg Ala Leu Asp Ala Gln Pro Ala Thr Leu Ala Ser Ser Trp
          565          570          575
Ser His Leu Gly Ala Lys Arg Cys Leu Lys Asn Arg Leu Glu Gln Cys
          580          585          590
His Leu Leu Glu Leu Glu Ala Ala Lys Asp Asp Tyr Gln Gly Ser Thr
          595          600          605
Asn Ser Pro Cys Gly Phe Ser Cys Leu
          610          615

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<210> 304
 <211> 72
 <212> PRT
 <213> Mouse

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<400> 304
Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
1          5          10          15
Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
          20          25          30
Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
          35          40          45
Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
          50          55          60

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1011c2PCTSEQUENCE LISTING

Ala Phe Ser Ile Leu Phe Ile Gln
65 70

<210> 305
<211> 649
<212> PRT
<213> Mouse

<400> 305
Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
1 5 10 15
Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
20 25 30
Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
35 40 45
Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
50 55 60
Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
65 70 75 80
Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
85 90 95
Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln
100 105 110
Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro
115 120 125
Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser
130 135 140
Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe
145 150 155 160
Leu Ser Arg Asn His Leu Ser Thr Ile Pro Gly Gly Leu Pro Arg Thr
165 170 175
Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser
180 185 190
Pro Ser Leu His Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly
195 200 205
Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu
210 215 220
Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
225 230 235 240
Pro Val Asn Leu Pro Gly Thr Ser Leu Arg Lys Leu Tyr Leu Gln Asp
245 250 255
Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln
260 265 270
Leu Tyr Arg Leu Asp Met Ser Asn Asn Leu Ser Asn Leu Pro Gln
275 280 285
Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn
290 295 300
Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu
305 310 315 320
Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala
325 330 335
Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Ser Ala Glu Leu
340 345 350
Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr
355 360 365

1011c2PCTSEQUENCE LISTING

Ala Ile Pro Asn Thr Ala Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro
 370 375 380
 Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Ile Lys Asp Gln
 385 390 395 400
 Arg Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Leu Ile Thr Val Lys
 405 410 415
 Ser Val Thr Pro Asp Thr Ile His Ile Ser Trp Arg Leu Ala Leu Pro
 420 425 430
 Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala
 435 440 445
 Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr
 450 455 460
 Leu Val Thr Ala Leu Glu Pro Glu Ser Pro Tyr Arg Val Cys Met Val
 465 470 475 480
 Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys
 485 490 495
 Ile Glu Thr Gln Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr
 500 505 510
 Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro
 515 520 525
 Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Ser Ile Ala Leu
 530 535 540
 Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser
 545 550 555 560
 Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala
 565 570 575
 Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr
 580 585 590
 Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu
 595 600 605
 Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys
 610 615 620
 Asn Asn Leu Ser Glu Ser Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly
 625 630 635 640
 Ile Pro Asp Ser Asp His Ser His Ser
 645

<210> 306

<211> 150

<212> PRT

<213> Rat

<400> 306

Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1 5 10 15
 Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
 20 25 30
 Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
 35 40 45
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Asp Ala
 50 55 60
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
 65 70 75 80
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr
 85 90 95

1011c2PCTSEQUENCE LISTING

Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys Trp Ile Pro Arg Ala Ala
 100 105 110
 Gly Leu Cys Ser Trp Cys Gly Gly Gly Leu Cys Val Arg Gly Ala His
 115 120 125
 Leu His Ala Leu Asp Glu His Gly Gly Gln Leu Leu Arg Pro Leu Arg
 130 135 140
 Val Arg Ser Arg Leu Leu
 145 150

<210> 307

<211> 580

<212> PRT

<213> Rat

<400> 307

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
 1 5 10 15
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
 20 25 30
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala
 35 40 45
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
 50 55 60
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
 65 70 75 80
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
 85 90 95
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
 100 105 110
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
 115 120 125
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
 130 135 140
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
 145 150 155 160
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
 165 170 175
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
 180 185 190
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
 195 200 205
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
 210 215 220
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
 225 230 235 240
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
 245 250 255
 Lys Lys Asp Trp Ser Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu
 260 265 270
 Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp Ile Thr Gly
 275 280 285
 Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser Pro Pro Pro Thr Ser
 290 295 300
 Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Val Tyr
 305 310 315 320

1011c2PCTSEQUENCE LISTING

Asp Leu Phe Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
 325 330 335
 Gln Leu Lys Trp Lys Arg Pro Pro Asp Asn Glu Ala Leu Pro Val Pro
 340 345 350
 Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly
 355 360 365
 Glu Leu Ser Thr Leu Leu Tyr Asn Ser His Pro Tyr Arg Ala Phe Pro
 370 375 380
 Val Leu Leu Leu Asp Ala Val Pro Trp Tyr Leu Arg Leu Tyr Val His
 385 390 395 400
 Thr Leu Thr Ile Thr Ser Lys Gly Lys Asp Asn Lys Pro Ser Tyr Ile
 405 410 415
 His Tyr Gln Pro Ala Gln Asp Arg Gln Gln Pro His Leu Leu Glu Met
 420 425 430
 Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe
 435 440 445
 Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His
 450 455 460
 Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met
 465 470 475 480
 Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Thr
 485 490 495
 Leu Phe Pro Val Ser Asp Gly Ser Ser Tyr Phe Val Arg Leu Tyr Thr
 500 505 510
 Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr
 515 520 525
 Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser
 530 535 540
 Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Lys Ser
 545 550 555 560
 Gly Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
 565 570 575
 Val Pro Pro Leu
 580

<210> 308

<211> 283

<212> PRT

<213> Rat

<400> 308

Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
 1 5 10 15
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20 25 30
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35 40 45
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50 55 60
 Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr
 65 70 75 80
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85 90 95
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
 100 105 110

1011c2PCTSEQUENCE LISTING

Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
 115 120 125
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
 130 135 140
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
 145 150 155 160
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
 165 170 175
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser
 180 185 190
 Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro
 195 200 205
 Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser
 210 215 220
 Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser
 225 230 235 240
 Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr
 245 250 255
 Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val
 260 265 270
 Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val
 275 280

<210> 309

<211> 37

<212> PRT

<213> Rat

<400> 309

Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
 1 5 10 15
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
 20 25 30
 Arg Ala Asp Val Leu
 35

<210> 310

<211> 70

<212> PRT

<213> Mouse

<400> 310

Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
 1 5 10 15
 Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu
 20 25 30
 Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile
 35 40 45
 Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu
 50 55 60
 Pro Leu Lys Ile Ser Pro
 65 70

<210> 311

<211> 58

1011c2PCTSEQUENCE LISTING

<212> PRT

<213> Human

<400> 311

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu	Ala
1				5					10					15	
Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys	Ile	Thr
			20					25					30		
Thr	Tyr	Ala	Ile	Asn	Val	Ser	Leu	Met	Trp	Leu	Ser	Phe	Arg	Lys	Val
		35					40					45			
Gln	Glu	Pro	Gln	Gly	Lys	Ala	Lys	Arg	His						
	50						55								

<210> 312

<211> 52

<212> PRT

<213> Human

<400> 312

Met	Gly	Thr	Pro	Gln	Gly	Glu	Asn	Trp	Leu	Ser	Trp	Met	Phe	Glu	Lys
1				5					10					15	
Leu	Val	Val	Val	Met	Val	Cys	Tyr	Phe	Ile	Leu	Ser	Ile	Ile	Asn	Ser
			20					25					30		
Met	Ala	Gln	Ser	Tyr	Ala	Lys	Arg	Ile	Gln	Gln	Arg	Leu	Asn	Ser	Glu
		35					40					45			
Glu	Lys	Thr	Lys												
	50														

<210> 313

<211> 70

<212> PRT

<213> Human

<400> 313

Met	Asn	Leu	Leu	Gly	Met	Ile	Phe	Ser	Met	Cys	Gly	Leu	Met	Leu	Lys
1				5					10					15	
Leu	Lys	Trp	Cys	Ala	Trp	Val	Ala	Val	Tyr	Cys	Ser	Phe	Ile	Ser	Phe
			20					25					30		
Ala	Asn	Ser	Arg	Ser	Ser	Glu	Asp	Thr	Lys	Gln	Met	Met	Ser	Ser	Phe
		35					40					45			
Met	Leu	Ser	Ile	Ser	Ala	Val	Val	Met	Ser	Tyr	Leu	Gln	Asn	Pro	Gln
	50					55					60				
Pro	Met	Thr	Pro	Pro	Trp										
65					70										

<210> 314

<211> 58

<212> PRT

<213> Mouse

<400> 314

Met	Phe	Ile	Thr	Pro	Phe	Lys	Ala	Phe	Leu	Pro	Leu	Tyr	Leu	Leu	Thr
1				5					10					15	
Glu	Leu	Ser	Leu	Ile	Asp	Ile	Thr	Ser	Cys	Asp	Asp	Leu	Pro	His	Ser
			20					25					30		

1011c2PCTSEQUENCE LISTING

Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr
 35 40 45
 Leu Leu Ile Cys Cys Phe Val Ile Ile Phe
 50 55

<210> 315
 <211> 229
 <212> PRT
 <213> Rat

<400> 315
 Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1 5 10 15
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20 25 30
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35 40 45
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50 55 60
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65 70 75 80
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85 90 95
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100 105 110
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115 120 125
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130 135 140
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145 150 155 160
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
 165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe
 225

<210> 316
 <211> 128
 <212> PRT
 <213> Rat

<400> 316
 Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly
 1 5 10 15
 Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr
 20 25 30
 Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp
 35 40 45
 Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro

1011c2PCTSEQUENCE LISTING

50		55		60												
Met	Phe	Val	Ile	Ala	Phe	Leu	Thr	Pro	Leu	Ser	Leu	Ile	Phe	Phe	Ala	
65					70					75					80	
Lys	Phe	Leu	Arg	Lys	Ala	Asp	Ala	Thr	Asp	Ser	Lys	Gln	Ala	Cys	Leu	
				85					90					95		
Ala	Ala	Ser	Leu	Ala	Leu	Ala	Leu	Asn	Gly	Val	Phe	Thr	Asn	Ile	Ile	
			100					105					110			
Lys	Leu	Ile	Val	Gly	Arg	Pro	Arg	Pro	Asp	Phe	Phe	Tyr	Arg	Cys	Phe	
		115					120					125				

<210> 317
 <211> 75
 <212> PRT
 <213> Rat

<400> 317

Ser	Ala	Gly	Val	Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	
1				5					10					15		
Ala	Phe	Gly	Pro	Ala	Leu	Ser	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Thr	Asp	
			20					25					30			
Pro	Leu	Arg	Val	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	
		35					40					45				
Ser	Leu	Leu	Leu	Ser	Ser	Val	Phe	Trp	Phe	Leu	Val	Arg	Val	Ile	Thr	
		50				55					60					
Asp	Asn	Arg	Asp	Gly	Pro	Val	Gln	Asn	Tyr	Leu						
65					70					75						

<210> 318
 <211> 43
 <212> PRT
 <213> Human

<400> 318

Met	Lys	Leu	Ser	Gly	Met	Phe	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Phe	Cys	
1				5					10					15		
Phe	Leu	Thr	Gly	Val	Phe	Ser	Gln	Gly	Gly	Gln	Val	Asp	Cys	Gly	Glu	
			20					25					30			
Ser	Arg	Thr	Pro	Arg	Pro	Thr	Ala	Leu	Gly	Asn						
		35					40									

<210> 319
 <211> 86
 <212> PRT
 <213> Mouse

<400> 319

Met	Leu	Gln	Gly	Pro	Ala	Pro	Ser	Cys	Phe	Trp	Val	Phe	Ser	Gly	Ile	
1				5					10					15		
Cys	Val	Phe	Trp	Asp	Phe	Ile	Phe	Ile	Ile	Phe	Phe	Asn	Val	Leu	Ser	
			20					25					30			
Leu	Gly	Asn	Arg	Glu	Ile	Ser	Ala	Lys	Asp	Phe	Ala	Asp	Gln	Pro	Ala	
		35					40					45				
Gly	Ala	Gln	Gly	Met	Trp	Gly	Ile	Trp	Gly	His	Thr	Ile	Thr	Cys	Gly	
		50				55					60					
Leu	Ala	Pro	Gly	Ala	Lys	Pro	Cys	Ser	Leu	Lys	Arg	Glu	Gly	Pro	Asp	

1011c2PCTSEQUENCE LISTING

65 70 75 80
Leu Leu Ser Phe Pro Pro
 85

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<210> 320
<211> 60
<212> PRT
<213> Mouse
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	<400> 320														
Lys	Gly	Pro	Glu	Val	Ser	Cys	Cys	Ile	Lys	Tyr	Phe	Ile	Phe	Gly	Phe
1				5					10					15	
Asn	Val	Ile	Phe	Trp	Phe	Leu	Gly	Ile	Thr	Phe	Leu	Gly	Ile	Gly	Leu
			20					25					30		
Trp	Ala	Trp	Asn	Glu	Lys	Gly	Val	Leu	Ser	Asn	Ile	Ser	Ser	Ile	Thr
		35					40					45			
Asp	Leu	Gly	Gly	Phe	Asp	Pro	Val	Trp	Leu	Phe	Leu				
	50					55					60				

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<210> 321
<211> 160
<212> PRT
<213> Mouse
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<400> 321															
Ile 1	Arg	His	Glu	Ala 5	Glu	Ala	Gly	Arg	His 10	Gln	Pro	Glu	Gln	Leu 15	Ala
Ala	Asp	Ser	Arg 20	Thr	Glu	Thr	Val	Gly 25	Pro	Arg	Gln	Ser	Asn 30	Gly	Leu
Thr	Gly	Pro 35	Gly	Leu	Pro	Thr	Trp 40	Gln	Leu	His	Pro	Val 45	Leu	Phe	Pro
Glu 50	Leu	Val	Leu	Trp	Val	Asn 55	Met	Val	Pro	Cys	Phe 60	Leu	Leu	Ser	Leu
Leu 65	Leu	Leu	Val	Arg	Pro 70	Ala	Pro	Val	Val	Ala 75	Tyr	Ser	Val	Ser	Leu 80
Pro	Ala	Ser	Phe 85	Leu	Glu	Glu	Val	Ala	Gly 90	Ser	Gly	Glu	Ala	Glu 95	Gly
Ser	Ser	Ala	Ser 100	Ser	Pro	Ser	Leu	Leu 105	Pro	Pro	Arg	Thr 110	Pro	Ala	Phe
Ser	Pro	Thr 115	Pro	Gly	Arg	Thr	Gln 120	Pro	Thr	Ala	Pro	Val 125	Gly	Pro	Val
Pro 130	Pro	Thr	Asn	Leu	Leu	Asp 135	Gly	Ile	Val	Asp	Phe 140	Phe	Arg	Gln	Tyr
Val 145	Met	Leu	Ile	Ala	Val 150	Val	Gly	Ser	Leu	Thr 155	Phe	Leu	Ile	Ser	Ser 160

<210>	322
<211>	54
<212>	PRT
<213>	Mouse

<400> 322
 Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Val Leu Phe Leu Phe Phe
 1 5 10 15
 Phe Phe Phe Leu Cys Val Cys Val Leu Val Cys Cys Cys Phe Gly Phe

1011c2PCTSEQUENCE LISTING

20 25 30
 Pro Gly Thr His Ser Val Asp Gln Ala Ser Pro Lys Leu Arg Asn Leu
 35 40 45
 Pro Pro Glu Cys Trp Asp
 50

<210> 323
 <211> 280
 <212> PRT
 <213> Mouse

<400> 323
 Leu Asp Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser
 1 5 10 15
 Ala Arg Glu Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile
 20 25 30
 Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile
 35 40 45
 Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro
 50 55 60
 His His His His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu
 65 70 75 80
 Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val
 85 90 95
 Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg
 100 105 110
 Lys Phe Val His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala
 115 120 125
 Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe
 130 135 140
 Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala
 145 150 155 160
 Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met
 165 170 175
 Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp
 180 185 190
 Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly
 195 200 205
 Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp
 210 215 220
 Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys
 225 230 235 240
 Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu
 245 250 255
 Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys
 260 265 270
 Ala Met Pro Ser Asp Met Asp Ser
 275 280

<210> 324
 <211> 166
 <212> PRT
 <213> Rat

<400> 324

1011c2PCTSEQUENCE LISTING

Ala	Leu	Arg	Arg	Val	Gly	Met	Glu	Leu	Pro	Ala	Val	Asn	Leu	Lys	Val
1				5					10					15	
Ile	Leu	Leu	Val	His	Trp	Leu	Leu	Thr	Thr	Trp	Gly	Cys	Leu	Ala	Phe
			20					25					30		
Ser	Gly	Ser	Tyr	Ala	Trp	Gly	Asn	Phe	Thr	Ile	Leu	Ala	Leu	Gly	Val
		35					40					45			
Trp	Ala	Val	Ala	Gln	Arg	Asp	Ser	Val	Asp	Ala	Ile	Gly	Met	Phe	Leu
	50					55					60				
Gly	Gly	Leu	Val	Ala	Thr	Ile	Phe	Leu	Asp	Ile	Ile	Tyr	Ile	Ser	Ile
65					70					75				80	
Phe	Tyr	Ser	Ser	Val	Ala	Val	Gly	Asp	Thr	Gly	Arg	Phe	Ser	Ala	Gly
				85					90					95	
Met	Ala	Ile	Phe	Ser	Leu	Leu	Leu	Lys	Pro	Phe	Ser	Cys	Cys	Leu	Val
			100					105					110		
Tyr	His	Met	His	Arg	Glu	Arg	Gly	Gly	Glu	Leu	Pro	Leu	Arg	Ser	Asp
		115					120					125			
Phe	Phe	Gly	Pro	Ser	Gln	Glu	His	Ser	Ala	Tyr	Gln	Thr	Ile	Asp	Ser
	130					135					140				
Ser	Asp	Ser	Pro	Ala	Asp	Pro	Leu	Ala	Ser	Leu	Glu	Asn	Lys	Gly	Gln
145					150					155					160
Ala	Ala	Pro	Arg	Gly	Tyr										
				165											

<210> 325

<211> 338

<212> PRT

<213> Rat

<400> 325

Ile	Arg	His	Glu	Ala	Glu	Ala	Gly	Arg	His	Gln	Pro	Glu	Gln	Leu	Ala
1				5					10					15	
Ala	Asp	Ser	Arg	Thr	Glu	Thr	Val	Gly	Pro	Arg	Gln	Ser	Asn	Gly	Leu
			20					25					30		
Thr	Gly	Pro	Gly	Leu	Pro	Thr	Trp	Gln	Leu	His	Pro	Val	Leu	Phe	Pro
		35					40					45			
Glu	Leu	Val	Leu	Trp	Val	Asn	Met	Val	Pro	Cys	Phe	Leu	Leu	Ser	Leu
	50					55				60					
Leu	Leu	Leu	Val	Arg	Pro	Ala	Pro	Val	Val	Ala	Tyr	Ser	Val	Ser	Leu
65					70					75				80	
Pro	Ala	Ser	Phe	Leu	Glu	Glu	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly
			85						90					95	
Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Leu	Pro	Pro	Arg	Thr	Pro	Ala	Phe
			100					105					110		
Ser	Pro	Thr	Pro	Gly	Arg	Thr	Gln	Pro	Thr	Ala	Pro	Val	Gly	Pro	Val
		115					120					125			
Pro	Pro	Thr	Asn	Leu	Leu	Asp	Gly	Ile	Val	Asp	Phe	Phe	Arg	Gln	Tyr
	130					135					140				
Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Thr	Phe	Leu	Ile	Met	Phe
145					150					155					160
Ile	Val	Cys	Ala	Ala	Leu	Ile	Thr	Arg	Gln	Lys	His	Lys	Ala	Thr	Ala
				165					170					175	
Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Glu	Lys	Lys	Tyr	Val	Asp	Gln	Arg	Asp
			180					185					190		
Arg	Ala	Gly	Gly	Pro	His	Ala	Phe	Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro
		195					200					205			

1011c2PCTSEQUENCE LISTING

Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala
 210 215 220
 Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu
 225 230 235 240
 Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu
 245 250 255
 Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg
 260 265 270
 Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp
 275 280 285
 Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly
 290 295 300
 Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly
 305 310 315 320
 Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro
 325 330 335
 Asn Val

<210> 326
 <211> 347
 <212> PRT
 <213> Human

<400> 326

Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala
 1 5 10 15
 Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser
 20 25 30
 Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp
 35 40 45
 Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly
 50 55 60
 Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp
 65 70 75 80
 Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser
 85 90 95
 Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu
 100 105 110
 Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala
 115 120 125
 Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val
 130 135 140
 Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala
 145 150 155 160
 Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Thr Tyr Val Leu Phe
 165 170 175
 Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser
 180 185 190
 Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu
 195 200 205
 Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro
 210 215 220
 Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala
 225 230 235 240

1011c2PCTSEQUENCE LISTING

Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp
 245 250 255
 Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala
 260 265 270
 Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg
 275 280 285
 Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp
 290 295 300
 Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro
 305 310 315 320
 Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro
 325 330 335
 Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser
 340 345

<210> 327
 <211> 141
 <212> PRT
 <213> Human

<400> 327

Lys Asn Ser Lys Cys Leu Leu Phe Trp Cys Arg Lys Ile Val Gly Asn
 1 5 10 15
 Arg Gln Glu Pro Met Trp Glu Phe Asn Phe Lys Phe Lys Lys Gln Ser
 20 25 30
 Pro Arg Leu Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln
 35 40 45
 Tyr Glu Asp Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln
 50 55 60
 Val Thr Thr Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile
 65 70 75 80
 Phe Thr Leu Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg
 85 90 95
 Val Arg Leu Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu
 100 105 110
 Arg Ser Glu Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe
 115 120 125
 Gly Ser Leu Thr Gly Gly Ile Leu Ser Thr His Ser Pro
 130 135 140

<210> 328
 <211> 71
 <212> PRT
 <213> Human

<400> 328

Arg Glu Arg Thr Ser Leu Glu Phe Phe Val Phe Leu Phe Leu Phe Ile
 1 5 10 15
 Cys Cys Cys Leu His Ser Gly Gly Leu Gly Gly Val Pro Leu Pro Pro
 20 25 30
 Phe Pro Pro Gln Ala Gln Arg Gly Glu Gly Pro Gly Lys Trp Met Ser
 35 40 45
 Pro Pro Leu Pro Pro His Pro Val Val Ala Pro Pro Thr Pro Ser Pro
 50 55 60
 Ser Arg Gly Cys Val Leu Leu

1011c2PCTSEQUENCE LISTING
70

65

<210> 329
 <211> 109
 <212> PRT
 <213> Human

<400> 329
 Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala Pro
 1 5 10 15
 Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His Ser
 20 25 30
 Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
 35 40 45
 Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
 50 55 60
 Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
 65 70 75 80
 Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg
 85 90 95
 Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
 100 105

<210> 330
 <211> 155
 <212> PRT
 <213> Human

<400> 330
 Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
 1 5 10 15
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
 20 25 30
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
 35 40 45
 Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
 50 55 60
 Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
 65 70 75 80
 Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
 85 90 95
 Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
 100 105 110
 Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val
 115 120 125
 Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe
 130 135 140
 Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
 145 150 155

<210> 331
 <211> 299
 <212> PRT
 <213> Human

1011c2PCTSEQUENCE LISTING

<400> 331

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile	
1				5					10					15		
Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His	
			20					25					30			
Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	
		35					40					45				
Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe	
	50				55						60					
Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	
65				70					75					80		
Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe	
				85				90						95		
Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	
			100					105					110			
Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly	Glu	Val	Lys	Val	Lys	Leu	Ile	Val	
		115					120					125				
Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	
	130				135						140					
Ile	Gly	Asn	Arg	Ala	Val	Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	
145				150					155						160	
Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	
			165					170						175		
Pro	Lys	Ser	Thr	Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	
			180					185					190			
Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	
		195					200					205				
Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	
	210				215						220					
Asn	Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val	
225				230					235						240	
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	
			245					250						255		
Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	Lys	Gly	
		260					265						270			
Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	
		275					280					285				
Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val						
	290					295										

<210> 332
 <211> 299
 <212> PRT
 <213> Mouse

<400> 332

Ala	Arg	Ala	Gly	Ala	Cys	Tyr	Cys	Pro	Ala	Gly	Phe	Leu	Gly	Ala	Asp	
1				5					10					15		
Cys	Ser	Leu	Ala	Cys	Pro	Gln	Gly	Arg	Phe	Gly	Pro	Ser	Cys	Ala	His	
			20					25					30			
Val	Cys	Thr	Cys	Gly	Gln	Gly	Ala	Ala	Cys	Asp	Pro	Val	Ser	Gly	Thr	
		35				40						45				
Cys	Ile	Cys	Pro	Pro	Gly	Lys	Thr	Gly	Gly	His	Cys	Glu	Arg	Gly	Cys	
	50				55					60						
Pro	Gln	Asp	Arg	Phe	Gly	Lys	Gly	Cys	Glu	His	Lys	Cys	Ala	Cys	Arg	

1011c2PCTSEQUENCE LISTING

65	Asn	Gly	Gly	Leu	Cys	His	Ala	Thr	Asn	Gly	Ser	Cys	Ser	Cys	Pro	Leu	80
					85					90					95		
	Gly	Trp	Met	Gly	Pro	His	Cys	Glu	His	Ala	Cys	Pro	Ala	Gly	Arg	Tyr	
			100					105						110			
	Gly	Ala	Ala	Cys	Leu	Leu	Glu	Cys	Ser	Cys	Gln	Asn	Asn	Gly	Ser	Cys	
			115					120					125				
	Glu	Pro	Thr	Ser	Gly	Ala	Cys	Leu	Cys	Gly	Pro	Gly	Phe	Tyr	Gly	Gln	
		130					135					140					
	Ala	Cys	Glu	Asp	Thr	Cys	Pro	Ala	Gly	Phe	His	Gly	Ser	Gly	Cys	Gln	
145						150				155						160	
	Arg	Val	Cys	Glu	Cys	Gln	Gln	Gly	Ala	Pro	Cys	Asp	Pro	Val	Ser	Gly	
				165						170					175		
	Arg	Cys	Leu	Cys	Pro	Ala	Gly	Phe	Arg	Gly	Gln	Phe	Cys	Glu	Arg	Gly	
			180						185					190			
	Cys	Lys	Pro	Gly	Phe	Phe	Gly	Asp	Gly	Cys	Leu	Gln	Gln	Cys	Asn	Cys	
		195					200					205					
	Pro	Thr	Gly	Val	Pro	Cys	Asp	Pro	Ile	Ser	Gly	Leu	Cys	Leu	Cys	Pro	
		210					215					220					
	Pro	Gly	Arg	Ala	Gly	Thr	Thr	Cys	Asp	Leu	Asp	Cys	Arg	Arg	Gly	Arg	
225						230					235					240	
	Phe	Gly	Pro	Gly	Cys	Ala	Leu	Arg	Cys	Asp	Cys	Gly	Gly	Gly	Ala	Asp	
				245						250					255		
	Cys	Asp	Pro	Ile	Ser	Gly	Gln	Cys	His	Cys	Val	Asp	Ser	Tyr	Thr	Gly	
			260						265					270			
	Pro	Thr	Cys	Arg	Glu	Val	Pro	Thr	Gln	Leu	Ser	Ser	Ile	Arg	Pro	Ala	
		275						280					285				
	Pro	Gln	His	Ser	Ser	Ser	Lys	Ala	Met	Lys	His						
		290					295										

<210> 333
 <211> 109
 <212> PRT
 <213> Mouse

	<400>	333															
	Gly	Thr	Arg	Val	Gly	Thr	Pro	Tyr	Tyr	Met	Ser	Pro	Glu	Arg	Ile	His	
1					5					10					15		
	Glu	Asn	Gly	Tyr	Asn	Phe	Lys	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Leu	
			20						25					30			
	Leu	Tyr	Glu	Met	Ala	Ala	Leu	Gln	Ser	Pro	Phe	Tyr	Gly	Asp	Lys	Met	
			35					40					45				
	Asn	Leu	Tyr	Ser	Leu	Cys	Lys	Lys	Ile	Glu	Gln	Cys	Asp	Tyr	Pro	Pro	
		50					55					60					
	Leu	Pro	Ser	Asp	His	Tyr	Ser	Glu	Glu	Leu	Arg	Gln	Leu	Val	Asn	Ile	
65						70					75					80	
	Cys	Ile	Asn	Pro	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Ile	Ala	Tyr	Val	Tyr	
				85						90					95		
	Asp	Val	Ala	Lys	Arg	Met	His	Ala	Cys	Thr	Ala	Ser	Thr				
			100						105								

<210> 334
 <211> 787
 <212> PRT
 <213> Mouse

1011c2PCTSEQUENCE LISTING

<400> 334

Lys	Val	Glu	Gly	Glu	Gly	Arg	Gly	Arg	Trp	Ala	Leu	Gly	Leu	Leu	Arg
1				5					10					15	
Thr	Phe	Asp	Ala	Gly	Glu	Phe	Ala	Gly	Trp	Glu	Lys	Val	Gly	Ser	Gly
			20					25					30		
Gly	Phe	Gly	Gln	Val	Tyr	Lys	Val	Arg	His	Val	His	Trp	Lys	Thr	Trp
		35				40						45			
Leu	Ala	Ile	Lys	Cys	Ser	Pro	Ser	Leu	His	Val	Asp	Asp	Arg	Glu	Arg
	50				55						60				
Met	Glu	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Met	Glu	Met	Ala	Lys	Phe	Arg
65				70						75				80	
Tyr	Ile	Leu	Pro	Val	Tyr	Gly	Ile	Cys	Gln	Glu	Pro	Val	Gly	Leu	Val
			85					90						95	
Met	Glu	Tyr	Met	Glu	Thr	Gly	Ser	Leu	Glu	Lys	Leu	Leu	Ala	Ser	Glu
			100					105					110		
Pro	Leu	Pro	Trp	Asp	Leu	Arg	Phe	Arg	Ile	Val	His	Glu	Thr	Ala	Val
		115					120					125			
Gly	Met	Asn	Phe	Leu	His	Cys	Met	Ser	Pro	Pro	Leu	Leu	His	Leu	Asp
	130					135					140				
Leu	Lys	Pro	Ala	Asn	Ile	Leu	Leu	Asp	Ala	His	Tyr	His	Val	Lys	Ile
145				150						155					160
Ser	Asp	Phe	Gly	Leu	Ala	Lys	Cys	Asn	Gly	Met	Ser	His	Ser	His	Asp
			165					170						175	
Leu	Ser	Met	Asp	Gly	Leu	Phe	Gly	Thr	Ile	Ala	Tyr	Leu	Pro	Pro	Glu
			180					185					190		
Arg	Ile	Arg	Glu	Lys	Ser	Arg	Leu	Phe	Asp	Thr	Lys	His	Asp	Val	Tyr
		195					200					205			
Ser	Phe	Ala	Ile	Val	Ile	Trp	Gly	Val	Leu	Thr	Gln	Lys	Lys	Pro	Phe
	210				215						220				
Ala	Asp	Glu	Lys	Asn	Ile	Leu	His	Ile	Met	Met	Lys	Val	Val	Lys	Gly
225				230						235					240
His	Arg	Pro	Glu	Leu	Pro	Pro	Ile	Cys	Arg	Pro	Arg	Pro	Arg	Ala	Cys
			245					250						255	
Ala	Ser	Leu	Ile	Gly	Leu	Met	Gln	Arg	Cys	Trp	His	Ala	Asp	Pro	Gln
			260					265					270		
Val	Arg	Pro	Thr	Phe	Gln	Glu	Ile	Thr	Ser	Glu	Thr	Glu	Asp	Leu	Cys
		275					280					285			
Glu	Lys	Pro	Asp	Glu	Glu	Val	Lys	Asp	Leu	Ala	His	Glu	Pro	Gly	Glu
	290				295						300				
Lys	Ser	Ser	Leu	Glu	Ser	Lys	Ser	Glu	Ala	Arg	Pro	Glu	Ser	Ser	Arg
305				310						315					320
Leu	Lys	Arg	Ala	Ser	Ala	Pro	Pro	Phe	Asp	Asn	Asp	Cys	Ser	Leu	Ser
			325					330						335	
Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Ile	Ser	Gln	Thr	Leu	Glu	Gly
			340					345					350		
Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Glu	Cys	Lys	Leu	Pro	Ser	Ser	
		355					360					365			
Ser	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser	Ala	Phe
	370					375					380				
Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Ala	Ser	Thr
385				390						395					400
Gly	Asp	Leu	Gly	Pro	Thr	Asp	Ile	Gln	Lys	Lys	Lys	Leu	Val	Asp	Ala
			405					410						415	
Ile	Ile	Ser	Gly	Asp	Thr	Ser	Arg	Leu	Met	Lys	Ile	Leu	Gln	Pro	Gln

Asp	Val	Asp	Leu	Val	Leu	Asp	Ser	Ser	Ala	Ser	Leu	Leu	His	Leu	Ala
		435					440					445			
Val	Glu	Ala	Gly	Gln	Glu	Glu	Cys	Val	Lys	Trp	Leu	Leu	Leu	Asn	Asn
	450					455					460				
Ala	Asn	Pro	Asn	Leu	Thr	Asn	Arg	Lys	Gly	Ser	Thr	Pro	Leu	His	Met
465					470					475					480
Ala	Val	Glu	Arg	Lys	Gly	Arg	Gly	Ile	Val	Glu	Leu	Leu	Leu	Ala	Arg
				485					490					495	
Lys	Thr	Ser	Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala	Leu	His
			500				505						510		
Phe	Ala	Ala	Gln	Asn	Gly	Asp	Glu	Ala	Ser	Thr	Arg	Leu	Leu	Leu	Glu
		515				520						525			
Lys	Asn	Ala	Ser	Val	Asn	Glu	Val	Asp	Phe	Glu	Gly	Arg	Thr	Pro	Met
	530					535					540				
His	Val	Ala	Cys	Gln	His	Gly	Gln	Glu	Asn	Ile	Val	Arg	Thr	Leu	Leu
545					550					555					560
Arg	Arg	Gly	Val	Asp	Val	Gly	Leu	Gln	Gly	Lys	Asp	Ala	Trp	Leu	Pro
				565					570					575	
Leu	His	Tyr	Ala	Ala	Trp	Gln	Gly	His	Leu	Pro	Ile	Val	Lys	Leu	Leu
			580					585					590		
Ala	Lys	Gln	Pro	Gly	Val	Ser	Val	Asn	Ala	Gln	Thr	Leu	Asp	Gly	Arg
		595					600					605			
Thr	Pro	Leu	His	Leu	Ala	Ala	Gln	Arg	Gly	His	Tyr	Arg	Val	Ala	Arg
	610					615					620				
Ile	Leu	Ile	Asp	Leu	Cys	Ser	Asp	Val	Asn	Ile	Cys	Ser	Leu	Gln	Ala
625					630					635					640
Gln	Thr	Pro	Leu	His	Val	Ala	Ala	Glu	Thr	Gly	His	Thr	Ser	Thr	Ala
				645					650					655	
Arg	Leu	Leu	Leu	His	Arg	Gly	Ala	Gly	Lys	Glu	Ala	Leu	Thr	Ser	Glu
			660					665					670		
Gly	Tyr	Thr	Ala	Leu	His	Leu	Ala	Ala	Gln	Asn	Gly	His	Leu	Ala	Thr
		675					680					685			
Val	Lys	Leu	Leu	Ile	Glu	Glu	Lys	Ala	Asp	Val	Met	Ala	Arg	Gly	Pro
	690					695					700				
Leu	Asn	Gln	Thr	Ala	Leu	His	Leu	Ala	Ala	Ala	Arg	Gly	His	Ser	Glu
705					710					715					720
Val	Val	Glu	Glu	Leu	Val	Ser	Ala	Asp	Leu	Ile	Asp	Leu	Ser	Asp	Glu
				725					730					735	
Gln	Gly	Leu	Ser	Ala	Leu	His	Leu	Ala	Ala	Gln	Gly	Arg	His	Ser	Gln
			740					745					750		
Thr	Val	Glu	Thr	Leu	Leu	Lys	His	Gly	Ala	His	Ile	Asn	Leu	Gln	Ser
		755					760					765			

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<210> 335
<211> 194
<212> PRT
<213> Mouse
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Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser

1011c2PCTSEQUENCE LISTING

1				5				10					15				
Val	Glu	Lys	Asp	Ser	Val	Val	Cys	Glu	Cys	His	Pro	Gly	Trp	Thr	Gly		
			20					25					30				
Pro	Leu	Cys	Asp	Gln	Glu	Ala	Arg	Asp	Pro	Cys	Leu	Gly	His	Ser	Cys		
		35					40					45					
Arg	His	Gly	Thr	Cys	Met	Ala	Thr	Gly	Asp	Ser	Tyr	Val	Cys	Lys	Cys		
	50					55					60						
Ala	Glu	Gly	Tyr	Gly	Gly	Ala	Leu	Cys	Asp	Gln	Lys	Asn	Asp	Ser	Ala		
65					70					75					80		
Ser	Ala	Cys	Ser	Ala	Phe	Lys	Cys	His	His	Gly	Gln	Cys	His	Ile	Ser		
			85						90					95			
Asp	Arg	Gly	Glu	Pro	Tyr	Cys	Leu	Cys	Gln	Pro	Gly	Phe	Ser	Gly	His		
		100						105					110				
His	Cys	Glu	Gln	Glu	Asn	Pro	Cys	Met	Gly	Glu	Ile	Val	Arg	Glu	Ala		
	115						120					125					
Ile	Arg	Arg	Gln	Lys	Asp	Tyr	Ala	Ser	Cys	Ala	Thr	Ala	Ser	Lys	Val		
	130					135						140					
Pro	Ile	Met	Glu	Cys	Arg	Gly	Gly	Cys	Gly	Thr	Cys	Cys	Gln	Pro			
145					150					155				160			
Ile	Arg	Ser	Lys	Arg	Arg	Lys	Tyr	Val	Phe	Gln	Cys	Thr	Asp	Gly	Ser		
			165						170					175			
Ser	Phe	Val	Glu	Glu	Val	Glu	Arg	His	Leu	Glu	Cys	Gly	Cys	Arg	Ala		
			180					185					190				
Cys	Ser																

<210> 336
 <211> 274
 <212> PRT
 <213> Human

<400> 336

Tyr	Arg	Tyr	Cys	Gln	His	Arg	Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg		
1				5				10					15				
Cys	Gln	Cys	Glu	Pro	Gly	Phe	Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys		
			20					25				30					
Val	Asp	Val	Asn	Glu	Cys	Asp	Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys		
	35					40						45					
Phe	Asn	Ser	Tyr	Gly	Thr	Phe	Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu		
	50					55					60						
Leu	His	Arg	Asp	Gly	Phe	Ser	Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr		
65					70					75					80		
Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe		
			85						90					95			
Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys		
			100					105					110				
Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala		
	115						120					125					
Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn		
	130					135					140						
Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys		
145					150					155				160			
Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His		
			165						170					175			
Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe		

1011c2PCTSEQUENCE LISTING

			180					185					190			
Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	
		195					200					205				
Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	
	210					215					220					
Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	
225					230					235					240	
Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	
				245					250					255		
Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	
			260					265					270			
Thr	Phe															

<210> 337
 <211> 316
 <212> PRT
 <213> Mouse

<400> 337

His	Glu	Glu	Glu	Pro	Cys	Asn	Asn	Gly	Ser	Glu	Ile	Leu	Ala	Tyr	Asn	
1				5					10					15		
Ile	Asp	Leu	Gly	Asp	Ser	Cys	Ile	Thr	Val	Gly	Asn	Thr	Thr	Thr	His	
		20						25				30				
Val	Met	Lys	Asn	Leu	Leu	Pro	Glu	Thr	Thr	Tyr	Arg	Ile	Arg	Ile	Gln	
		35					40					45				
Ala	Ile	Asn	Glu	Ile	Gly	Val	Gly	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	
	50				55						60					
Lys	Thr	Arg	Pro	Leu	Pro	Pro	Ser	Pro	Pro	Arg	Leu	Glu	Cys	Ala	Ala	
65				70						75					80	
Ser	Gly	Pro	Gln	Ser	Leu	Lys	Leu	Lys	Trp	Gly	Asp	Ser	Asn	Ser	Lys	
				85					90					95		
Thr	His	Ala	Ala	Gly	Asp	Met	Val	Tyr	Thr	Leu	Gln	Leu	Glu	Asp	Arg	
			100					105					110			
Asn	Lys	Arg	Phe	Ile	Ser	Ile	Tyr	Arg	Gly	Pro	Ser	His	Thr	Tyr	Lys	
		115					120					125				
Val	Gln	Arg	Leu	Thr	Glu	Phe	Thr	Cys	Tyr	Ser	Phe	Arg	Ile	Gln	Ala	
	130					135					140					
Met	Ser	Glu	Ala	Gly	Glu	Gly	Pro	Tyr	Ser	Glu	Thr	Tyr	Thr	Phe	Ser	
145					150					155					160	
Thr	Thr	Lys	Ser	Val	Pro	Pro	Thr	Leu	Lys	Ala	Pro	Arg	Val	Thr	Gln	
				165					170					175		
Leu	Glu	Gly	Asn	Ser	Cys	Glu	Ile	Phe	Trp	Glu	Thr	Val	Pro	Pro	Met	
			180					185					190			
Arg	Gly	Asp	Pro	Val	Ser	Tyr	Val	Leu	Gln	Val	Leu	Val	Gly	Arg	Asp	
		195					200					205				
Ser	Glu	Tyr	Lys	Gln	Val	Tyr	Lys	Gly	Glu	Glu	Ala	Thr	Phe	Gln	Ile	
	210					215					220					
Ser	Gly	Leu	Gln	Ser	Asn	Thr	Asp	Tyr	Arg	Phe	Arg	Val	Cys	Ala	Cys	
225					230					235					240	
Arg	Arg	Cys	Val	Asp	Thr	Ser	Gln	Glu	Leu	Ser	Gly	Ala	Phe	Ser	Pro	
				245					250					255		
Ser	Ala	Ala	Phe	Met	Leu	Gln	Gln	Arg	Glu	Val	Met	Leu	Thr	Gly	Asp	
			260					265					270			
Leu	Gly	Gly	Met	Glu	Glu	Ala	Lys	Met	Lys	Gly	Met	Met	Pro	Thr	Asp	

1011c2PCTSEQUENCE LISTING

	275		280		285
Glu	Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile				
	290		295		300
Leu	Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys				
305		310		315	

<210> 338
 <211> 237
 <212> PRT
 <213> Mouse

<400> 338

Met	Leu	Ser	Leu	Arg	Ser	Leu	Leu	Pro	His	Leu	Gly	Leu	Phe	Leu	Cys
1				5					10					15	
Leu	Ala	Leu	His	Leu	Ser	Pro	Ser	Leu	Ser	Ala	Ser	Asp	Asn	Gly	Ser
			20					25					30		
Cys	Val	Val	Leu	Asp	Asn	Ile	Tyr	Thr	Ser	Asp	Ile	Leu	Glu	Ile	Ser
		35					40					45			
Thr	Met	Ala	Asn	Val	Ser	Gly	Gly	Asp	Val	Thr	Tyr	Thr	Val	Thr	Val
	50					55					60				
Pro	Val	Asn	Asp	Ser	Val	Ser	Ala	Val	Ile	Leu	Lys	Ala	Val	Lys	Glu
65					70					75				80	
Asp	Asp	Ser	Pro	Val	Gly	Thr	Trp	Ser	Gly	Thr	Tyr	Glu	Lys	Cys	Asn
			85						90					95	
Asp	Ser	Ser	Val	Tyr	Tyr	Asn	Leu	Thr	Ser	Gln	Ser	Gln	Ser	Val	Phe
			100					105						110	
Gln	Thr	Asn	Trp	Thr	Val	Pro	Thr	Ser	Glu	Asp	Val	Thr	Lys	Val	Asn
		115					120					125			
Leu	Gln	Val	Leu	Ile	Val	Val	Asn	Arg	Thr	Ala	Ser	Lys	Ser	Ser	Val
	130					135					140				
Lys	Met	Glu	Gln	Val	Gln	Pro	Ser	Ala	Ser	Thr	Pro	Ile	Pro	Glu	Ser
145					150					155				160	
Ser	Glu	Thr	Ser	Gln	Thr	Ile	Asn	Thr	Thr	Pro	Thr	Val	Asn	Thr	Ala
				165					170					175	
Lys	Thr	Thr	Ala	Lys	Asp	Thr	Ala	Asn	Thr	Thr	Ala	Val	Thr	Thr	Ala
			180				185						190		
Asn	Thr	Thr	Ala	Asn	Thr	Thr	Ala	Val	Thr	Thr	Ala	Lys	Thr	Thr	Ala
	195					200					205				
Lys	Ser	Leu	Ala	Ile	Arg	Thr	Leu	Gly	Ser	Pro	Leu	Ala	Gly	Ala	Leu
	210					215					220				
His	Ile	Leu	Leu	Val	Phe	Leu	Ile	Ser	Lys	Leu	Leu	Phe			
225					230					235					

<210> 339
 <211> 469
 <212> PRT
 <213> Mouse

<400> 339

Met	Leu	Cys	Leu	Cys	Leu	Tyr	Val	Pro	Ile	Ala	Gly	Ala	Ala	Gln	Thr
1				5					10					15	
Glu	Phe	Gln	Tyr	Phe	Glu	Ser	Lys	Gly	Leu	Pro	Ala	Glu	Leu	Lys	Ser
			20					25					30		
Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe	Ser	Thr	Tyr
		35					40					45			

1011c2PCTSEQUENCE LISTING

Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp	Lys	Asp	Leu	Asp		
50						55					60						
Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr	Leu	Gln	Asp	His	Glu		
65					70					75					80		
Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ser	Leu	Asp	Lys	Lys	Asn	Asp	Gly		
				85					90					95			
Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	Ser	Leu	Arg	Asp	Leu	Gly	Val		
			100					105					110				
Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys		
		115					120					125					
Asn	Gly	Thr	Met	Thr	Ile	Asp	Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu		
130						135					140						
Leu	His	Pro	Val	Glu	Asn	Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His		
145					150					155					160		
Ser	Thr	Ile	Phe	Asp	Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe		
				165					170					175			
Thr	Val	Glu	Glu	Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala		
			180					185					190				
Gly	Gly	Gly	Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp		
		195					200					205					
Arg	Leu	Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met		
210					215						220						
Cys	Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Lys		
225					230					235					240		
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	Glu		
				245					250					255			
Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Met	Lys	Arg	Leu	Val	Gly		
			260					265					270				
Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	Ala	Gly	Ser		
		275					280					285					
Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	Met	Glu	Val	Leu		
290					295						300						
Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	Tyr	Ser	Gly	Met	Leu		
305					310					315					320		
Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Lys	Glu	Gly	Val	Ala	Ala	Phe	Tyr		
				325					330					335			
Lys	Gly	Tyr	Ile	Pro	Asn	Met	Leu	Gly	Ile	Ile	Pro	Tyr	Ala	Gly	Ile		
			340					345					350				
Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	Lys	Asn	Thr	Trp	Leu	Gln	Arg	Tyr		
		355					360					365					
Ala	Val	Asn	Ser	Ala	Asp	Pro	Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly		
370					375						380						
Thr	Ile	Ser	Ser	Thr	Cys	Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu		
385					390					395					400		
Val	Arg	Thr	Arg	Met	Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu		
				405					410					415			
Val	Thr	Met	Ser	Ser	Leu	Phe	Lys	Gln	Ile	Leu	Arg	Thr	Glu	Gly	Ala		
			420					425					430				
Phe	Gly	Leu	Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro		
		435				440					445						
Ala	Val	Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu		
450					455						460						
Gly	Val	Gln	Ser	Arg													
465																	

1011c2PCTSEQUENCE LISTING

<210> 340
 <211> 99
 <212> PRT
 <213> Mouse

<400> 340
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20 25 30
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35 40 45
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
 50 55 60
 Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
 65 70 75 80
 Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
 85 90 95
 Tyr Glu Glu

<210> 341
 <211> 431
 <212> PRT
 <213> Mouse

<400> 341
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
 20 25 30
 Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
 85 90 95
 Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
 100 105 110
 Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
 115 120 125
 Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

1011c2PCTSEQUENCE LISTING

Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
 290 295 300
 Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly Ala Leu Leu Glu Gly Ala Arg Phe Met Gly Arg His Ser Glu
 325 330 335
 Phe Ala Leu His Ala Leu Leu Leu Ser Ile Cys Ser Ala Phe Gly Gln
 340 345 350
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 355 360 365
 Ile Ile Met Thr Leu Arg Gln Ala Ile Ala Ile Leu Leu Ser Cys Leu
 370 375 380
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400
 Val Phe Thr Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Lys Gln
 405 410 415
 Arg Gly Lys Lys Ala Val Pro Thr Glu Pro Pro Val Gln Lys Val
 420 425 430

<210> 342
 <211> 51
 <212> PRT
 <213> Mouse

<400> 342
 Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

<210> 343
 <211> 51
 <212> PRT
 <213> Human
 <400> 343

Leu Lys Phe Ser His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

1011c2PCTSEQUENCE LISTING

<210> 344
 <211> 95
 <212> PRT
 <213> Human

<400> 344
 Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val
 1 5 10 15
 Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr
 20 25 30
 Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu
 35 40 45
 Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly
 50 55 60
 Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile
 65 70 75 80
 Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 85 90 95

<210> 345
 <211> 77
 <212> PRT
 <213> Mouse

<400> 345
 Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1 5 10 15
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
 20 25 30
 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu
 35 40 45
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
 50 55 60
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 65 70 75

<210> 346
 <211> 77
 <212> PRT
 <213> Human

<400> 346
 Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1 5 10 15
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
 20 25 30
 Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
 35 40 45
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
 50 55 60
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 65 70 75

<210> 347

1011c2PCTSEQUENCE LISTING

<211> 215
 <212> PRT
 <213> Mouse

<400> 347

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Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1          5          10          15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
 20          25          30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
 35          40          45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
 50          55          60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
 65          70          75          80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
 85          90          95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100          105          110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115          120          125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130          135          140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145          150          155          160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165          170          175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180          185          190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195          200          205
Lys Ser Leu Ala Ile Arg Thr
210          215

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<210> 348
 <211> 21
 <212> PRT
 <213> Mouse

<400> 348

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Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val
 1          5          10          15
Pro Gln Phe Leu Asn

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<210> 349
 <211> 417
 <212> DNA
 <213> Mouse

<400> 349

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gctagccgtg caccagctc tccggagcgc gtgcaggcga gccgagcgcc ccgtccgcgg
 60
ttctcgggca ggcgctgcgg gctccccggc tccccgccgt cccgggcacc cgggcggggc
120
atgcgccccg gctagagcgt agccgccggc atgccgctcc cgctgctgct cgccgcgctc

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1011c2PCTSEQUENCE LISTING

180
 tgcctcgccg cctccccggc gcccgcgcg cctgcccagc tgccgtcgga gtggagaccc
 240
 ttgagcgaag gctgccgcg cgagctagcc gagaccatcg tgtatgccaa ggtgctggcg
 300
 ctgcaccccg aggtgcctgg cctctacaac tacctgccgt ggcagtacca agctggagag
 360
 ggagggtctt tctactccgc cgagggtggag atgcttgtgt gaccaaggcg tggggca
 417

<210> 350
 <211> 1837
 <212> DNA
 <213> Mouse

<400> 350
 cccccacctg ccagcccaag ccgagtgcg ccggctttgt tcgctttgtc ctgcgcacc
 60
 taagcgccg gcctggaaga acgccatccc ggagagcgca cgcggcgtcg caccaggtct
 120
 aacaacatgc ctccatttct gcttctacca gccatctaca tgctcctgtt cttcagagtg
 180
 tccccgacca tctctcttca ggaagtgcac gtgaaccggg agaccatggg gaagatcgct
 240
 gtggccagca aattaatgtg gtgctcagcc gcggtcgaca tcctgtttct gttagatggc
 300
 tctcacagca tcgggaaggg gagcttcgag aggtccaagc gcttcgccat cgctgcctgt
 360
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 420
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 720
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 780
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 840
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 900
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 960
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 1020
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 1080
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 1140
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1011c2PCTSEQUENCE LISTING

1200
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 1260
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 1320
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 1380
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 1440
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 1680
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 1740
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<210> 351
 <211> 941
 <212> DNA
 <213> Mouse

<400> 351
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 240
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 300
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 420
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 480
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 600
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 660
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 720
 gacttcata gacagacctt cagtgtcttt catgtccagg ccttgatctc tctagcetta

1011c2PCTSEQUENCE LISTING

780
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 840
 aatgaagttg atctaccagg gtcggctgct gcaggacca gcacgcacac tgagttccct
 900
 gaacattacc aacaactgcg tgatccactg ccaccgctca c
 941

<210> 352
 <211> 571
 <212> DNA
 <213> Mouse

<400> 352
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 120
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 420
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 480
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 571

<210> 353
 <211> 467
 <212> DNA
 <213> Rat

<400> 353
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 180
 aaggccatgt tctaccacgc ctacgacagt tacctggaaa atgcctttcc ctacgatgag
 240
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 300
 gatgccctgg acaccttget gattttgggg aatacctctg aattccaaag agtgggtggag
 360
 gttctccagg acaaacgtgg actttgatat cgacgtcaat gcctctgtgt tcgaaaccaa
 420

1011c2PCTSEQUENCE LISTING

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467

<210> 354

<211> 528

<212> DNA

<213> Rat

<400> 354

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120
tctcgagtgt ccactcccaa gccagcccc actggccata tggcatcata tctgggggtc
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240
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360
tatcctgttg ttaagctgtt tccacagaag cccgttcagg tagttacttc acccacattg
420
gccctatagc cagaggagtgt ccttggttaa ctgcagtgtg agcttgtaag caacagaagt
480
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528

<210> 355

<211> 473

<212> DNA

<213> Mouse

<400> 355

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120
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180
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240
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300
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360
ctgtgtggac atgcctgggc atgaaggcac caccgctcc tccctggatg acctgtccat
420
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473

<210> 356

<211> 431

<212> DNA

<213> Rat

1011c2PCTSEQUENCE LISTING

<400> 356

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 120
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 180
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 240
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 300
 ttgcaatgaa atctagaagg ggacctcatg tccctgtggg acacaatgcc ccgaaggact
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 431

<210> 357

<211> 1206

<212> DNA

<213> Mouse

<400> 357

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 120
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 180
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 240
 aataaaatca gcctgctagg gttcctgggc ctcgtccact gcctcccctg caaagattcc
 300
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 360
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 420
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 480
 gacttgccgc tcatgtaccg cggccgctgt caaaagtctt gcgctcaggc agtgtgcccg
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 600
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 660
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 720
 cggcaccag gcattctcac aggtggcccc aaagtaccag cagaggagga agagaacttc
 780
 gtgtgagctg cagccactgg gcctggcatt tgacgccatc ccgattttat ttattgttat
 840
 agaaaatatt ctaatttatg tcacatggac atttcccaaa cctggcctgg aaccacttgg
 900

1011c2PCTSEQUENCE LISTING

ggatccccct gggatcctga gcacgtatca caaggactga agggagattt ttataatagt
 960
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 1020
 agggatggca gctgcatgga gatccccctg ctatgatctc cccacctgct ttctaggctg
 1080
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 aacctg
 1206

<210> 358
 <211> 1052
 <212> DNA
 <213> Rat

<400> 358
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 360
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 480
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 660
 aacacctggc catcggccta gtgcacaatg gccagtaccg cattcggact tttgacgcca
 720
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 780
 aagtctggtt acagattttc tactcggagc agaatggact cttctacgac cttatttga
 840
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 900
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 960
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 1020
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 1052

1011c2PCTSEQUENCE LISTING

<210> 359
 <211> 1134
 <212> DNA
 <213> Rat

<400> 359
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 120
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 180
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 240
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 300
 cctgcatgtg gtggagccca tgccgggtgcc tggccatgat gtggaagcct actgctgtct
 360
 ctgtgagtgt aggtatgagg agcgcagcac cacaaccatc aaggtcatta tcgtcatcta
 420
 cctgtctgtg gtaggggccc tcttactcta catggccttc ctgatgctgg tggaccctct
 480
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 720
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 780
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 900
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 960
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 1020
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 1134

<210> 360
 <211> 876
 <212> DNA
 <213> Mouse

<400> 360
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1011c2PCTSEQUENCE LISTING

120
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 180
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 240
 aaccgcatct cccgaatccc cgtctccttc tgccgcctca ggcacctgca ggtcggttctg
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 420
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 660
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 720
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 780
 cgagaggagc ctgcagggga ggagaggcgg cgcacagaca ctttgcagtt gtggcaggaa
 840
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 876

<210> 361
 <211> 495
 <212> DNA
 <213> Mouse

<400> 361
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 120
 caacttggcg ggaaggaacc tcggggaagt ccctcagtgt gtttggagaa taaatgtgga
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 240
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 300
 ccgactcttg cctgccctta ctgttcttga tatacatgat aatcagctga catctcttcc
 360
 ttcagctata agagagctag acaatcttca gaaacttaat gtcagccata acaaactgaa
 420
 aatactgcct gaagaaatta caagcttaaa aaacctgagg acgctgcacc tccagcacia
 480
 tgagctgact tgcac
 495

<210> 362
 <211> 349

1011c2PCTSEQUENCE LISTING

<212> DNA

<213> Mouse

<400> 362

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120
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240
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349

<210> 363

<211> 380

<212> DNA

<213> Mouse

<400> 363

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120
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240
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300
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380

<210> 364

<211> 351

<212> DNA

<213> Mouse

<400> 364

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120
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180
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240
ggcatacgat gctaattagg gcacggatgc cctgctacac ccaaacttcc tcatccattt
300
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1011c2PCTSEQUENCE LISTING

351

<210> 365

<211> 854

<212> DNA

<213> Rat

<400> 365

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 120
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 480
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 720
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 780
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 840
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 854

<210> 366

<211> 257

<212> DNA

<213> Rat

<400> 366

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 120
 cggttcgggt catgcattgc ctccgttcaa gacctcaacc aagattccta caatgacgtg
 180
 gtgggtggggg cccctcagga ggacagccac agagggggcca tctacatctt ccatggcttc
 240
 caaaccaaca tcctgaa
 257

1011c2PCTSEQUENCE LISTING

<210> 367

<211> 475

<212> DNA

<213> Rat

<400> 367

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<212> DNA

<213> Mouse

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<212> DNA

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 35 40 45
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 35 40 45
 Ala Val Asp Ile Leu Phe Leu Leu Asp Gly Ser His Ser Ile Gly Lys
 50 55 60
 Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Ala Cys Asp Ala
 65 70 75 80
 Leu Asp Ile Ser Pro Gly Arg Val Arg Val Gly Ala Leu Gln Phe Gly
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 Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln
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 Glu Val Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr
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Cys	Tyr	Arg	Thr	Ile	Cys	Pro	Gly	Pro	Cys	Asp	Ser	Gln	Pro	Cys	Gln		
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Pro	Leu	His	His	Gly	Ala	Pro	Gly	Pro	Glu	Gly	Thr	Ala	Pro	Asp	Pro		
			20					25					30				
Ala	His	Tyr	Arg	Glu	Arg	Val	Lys	Ala	Met	Phe	Tyr	His	Ala	Tyr	Asp		
		35					40					45					
Ser	Tyr	Leu	Glu	Asn	Ala	Phe	Pro	Tyr	Asp	Glu	Leu	Arg	Pro	Leu	Thr		
	50					55					60						
Cys	Asp	Gly	His	Asp	Thr	Trp	Gly	Ser	Phe	Ser	Leu	Thr	Leu	Ile	Asp		
65					70					75					80		
Ala	Leu	Asp	Thr	Leu	Leu	Ile	Leu	Gly	Asn	Thr	Ser	Glu	Phe	Gln	Arg		
				85					90					95			
Val	Val	Glu	Val	Leu	Gln	Asp	Lys	Arg	Gly	Leu							
			100					105									

<210> 378
 <211> 95
 <212> PRT
 <213> Rat

Met	Trp	Phe	Leu	Pro	Cys	Ser	Val	Pro	Leu	Val	Ile	Ser	Ser	Cys	His		

1011c2PCTSEQUENCE LISTING

1	5	10	15
Ser Gln Ala	Ser Pro His Trp Pro Tyr Gly Ile Ile	Ser Gly Gly Gln	
	20	25	30
Glu Gly Leu	Cys Arg Leu Trp Thr Ala Thr Cys His	Ser Arg Gly Glu	
	35	40	45
Ser Glu Val	Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln		
	50	55	60
Gly Ser Leu	Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys		
65	70	75	80
Ala His Thr	Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys		
	85	90	95

<210> 379
 <211> 138
 <212> PRT
 <213> Mouse

<400> 379

Met Asp Leu Asp	Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1	5 10 15
Ala Ile Pro Ile	Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
	20 25 30
Ala Leu Ile Arg	Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
	35 40 45
Gln Val Arg Tyr	Ala His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
	50 55 60
Arg Gly Arg Pro	Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65	70 75 80
Ser Ala His Lys	Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
	85 90 95
Asn Leu His Leu	Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
	100 105 110
Arg Ser Ser Leu	Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile
	115 120 125
His Gln Phe Val	Glu Cys Leu Lys Leu Asn
130	135

<210> 380
 <211> 81
 <212> PRT
 <213> Rat

<400> 380

Met Ala Ser Ser	Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val
1	5 10 15
Met Ala Tyr Gly	Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys
	20 25 30
Arg Gln Ile Met	Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val
	35 40 45
Pro Val Gly His	Asn Ala Pro Lys Asp Leu Lys Glu Glu Ile Asp Ile
	50 55 60
Arg Leu Ser Arg	Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala
65	70 75 80
Asp	

1011c2PCTSEQUENCE LISTING

<210> 381
 <211> 257
 <212> PRT
 <213> Mouse

<400> 381
 Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp
 1 5 10 15
 Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro
 20 25 30
 Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu
 35 40 45
 Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn
 50 55 60
 Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser
 65 70 75 80
 Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser
 85 90 95
 Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly
 100 105 110
 Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro
 115 120 125
 Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu
 130 135 140
 Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val
 145 150 155 160
 Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro
 165 170 175
 Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val
 180 185 190
 Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu
 195 200 205
 Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg
 210 215 220
 Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly
 225 230 235 240
 Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe
 245 250 255
 Val

<210> 382
 <211> 285
 <212> PRT
 <213> Rat

<400> 382
 Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
 1 5 10 15
 Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro
 20 25 30
 Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
 35 40 45
 Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly

1011c2PCTSEQUENCE LISTING

50					55				60							
Lys	Asp	Gly	Gln	Asp	Gly	Gln	Asp	Gly	Asp	Arg	Gly	Asp	Ser	Gly	Glu	
65					70				75						80	
Glu	Gly	Pro	Pro	Gly	Arg	Thr	Gly	Asn	Arg	Gly	Lys	Gln	Gly	Pro	Lys	
				85					90					95		
Gly	Lys	Ala	Gly	Ala	Ile	Gly	Arg	Ala	Gly	Pro	Arg	Gly	Pro	Lys	Gly	
			100					105					110			
Val	Ser	Gly	Thr	Pro	Gly	Lys	His	Gly	Ile	Pro	Gly	Lys	Lys	Gly	Pro	
		115					120					125				
Lys	Gly	Lys	Lys	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Pro	Cys	Ser	Cys	Gly	
	130					135					140					
Ser	Ser	Arg	Ala	Lys	Ser	Ala	Phe	Ser	Val	Ser	Val	Thr	Lys	Ser	Tyr	
145					150				155						160	
Pro	Arg	Glu	Arg	Leu	Pro	Ile	Lys	Phe	Asp	Lys	Ile	Leu	Met	Asn	Glu	
				165					170					175		
Gly	Gly	His	Tyr	Asn	Ala	Ser	Ser	Gly	Lys	Phe	Val	Cys	Ser	Val	Pro	
			180					185					190			
Gly	Ile	Tyr	Tyr	Phe	Thr	Tyr	Asp	Ile	Thr	Leu	Ala	Asn	Lys	His	Leu	
		195					200					205				
Ala	Ile	Gly	Leu	Val	His	Asn	Gly	Gln	Tyr	Arg	Ile	Arg	Thr	Phe	Asp	
	210					215					220					
Ala	Asn	Thr	Gly	Asn	His	Asp	Val	Ala	Ser	Gly	Ser	Thr	Ile	Leu	Ala	
225					230					235					240	
Leu	Lys	Glu	Gly	Asp	Glu	Val	Trp	Leu	Gln	Ile	Phe	Tyr	Ser	Glu	Gln	
				245					250					255		
Asn	Gly	Leu	Phe	Tyr	Asp	Pro	Tyr	Trp	Thr	Asp	Ser	Leu	Phe	Thr	Gly	
		260					265						270			
Phe	Leu	Ile	Tyr	Ala	Asp	Gln	Gly	Asp	Pro	Asn	Glu	Val				
	275						280					285				

<210> 383

<211> 183

<212> PRT

<213> Rat

<400> 383

Met	Lys	Leu	Leu	Cys	Leu	Val	Ala	Val	Val	Gly	Cys	Leu	Leu	Val	Pro	
1				5					10					15		
Pro	Ala	Gln	Ala	Asn	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Cys	Lys	Cys	Ile	
			20					25					30			
Cys	Pro	Pro	Tyr	Arg	Asn	Ile	Ser	Gly	His	Ile	Tyr	Asn	Gln	Asn	Val	
		35					40					45				
Ser	Gln	Lys	Asp	Cys	Asn	Cys	Leu	His	Val	Val	Glu	Pro	Met	Pro	Val	
	50					55					60					
Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	Cys	Glu	Cys	Arg	Tyr	
65					70					75					80	
Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	Ile	Ile	Val	Ile	Tyr	Leu	
				85					90					95		
Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	Met	Ala	Phe	Leu	Met	Leu	Val	
			100					105					110			
Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	
		115					120					125				
Glu	Glu	Glu	Asn	Glu	Asp	Ala	Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	
	130					135					140					
Ile	Gly	Gly	Pro	Arg	Ala	Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	

1011c2PCTSEQUENCE LISTING

[illegible]

<210>	384
<211>	292
<212>	PRT
<213>	Mouse

<400> 384

[illegible]

<210>	385
<211>	164
<212>	PRT
<213>	Mouse

1011c2PCTSEQUENCE LISTING

<400> 385
 Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His
 1 5 10 15
 Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys
 20 25 30
 Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly
 35 40 45
 Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu
 50 55 60
 Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln
 65 70 75 80
 Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu
 85 90 95
 Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His
 100 105 110
 Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn
 115 120 125
 Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu
 130 135 140
 Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn
 145 150 155 160
 Glu Leu Thr Cys

<210> 386
 <211> 71
 <212> PRT
 <213> Mouse

<400> 386
 Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr
 1 5 10 15
 Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe
 20 25 30
 Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg
 35 40 45
 Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys
 50 55 60
 Val Gln Ser Ser Phe Leu Gly
 65 70

<210> 387
 <211> 126
 <212> PRT
 <213> Mouse

<400> 387
 Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg
 1 5 10 15
 Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro
 20 25 30
 Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr
 35 40 45
 Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala

1011c2PCTSEQUENCE LISTING

50		55		60											
Ala	Leu	Ala	Met	Asn	Ser	Ser	Pro	Ser	Val	Arg	Ser	Asn	Ile	Arg	Val
65					70					75					80
Thr	Val	Thr	Ala	Thr	Ala	Val	Ile	Ile	Asn	Leu	Val	Val	Ile	Ile	Leu
				85					90					95	
Leu	Asp	Glu	Val	Tyr	Gly	Cys	Ile	Ala	Arg	Trp	Leu	Thr	Lys	Ile	Gly
			100					105					110		
Glu	Cys	His	Val	Gln	Asp	Ser	Ile	Gly	Ser	Met	Gly	Leu	Gly		
		115					120					125			

<210> 388
 <211> 84
 <212> PRT
 <213> Rat

<400> 388

Ala	Ala	Glu	Asn	Glu	Met	Pro	Val	Ala	Val	Gly	Pro	Tyr	Gly	Gln	Ser
1				5					10					15	
Gln	Pro	Ser	Cys	Phe	Asp	Arg	Val	Lys	Met	Gly	Phe	Val	Met	Gly	Cys
			20					25					30		
Ala	Val	Gly	Met	Ala	Ala	Gly	Ala	Leu	Phe	Gly	Thr	Phe	Ser	Cys	Leu
		35				40						45			
Arg	Ile	Gly	Met	Arg	Gly	Arg	Glu	Leu	Met	Gly	Gly	Ile	Gly	Lys	Thr
	50				55					60					
Met	Met	Gln	Ser	Gly	Gly	Thr	Phe	Gly	Thr	Phe	Met	Ala	Ile	Gly	Met
65					70					75					80
Gly	Ile	Arg	Cys												

<210> 389
 <211> 284
 <212> PRT
 <213> Rat

<400> 389

Gly	Gly	Ser	Ser	Val	Ser	His	Val	Leu	Arg	Gly	Ser	Gly	Gln	Glu	Arg
1				5					10					15	
Ser	Pro	Pro	Pro	Ala	Ser	Met	Gln	Pro	Pro	Trp	Gly	Leu	Ala	Leu	Pro
			20					25					30		
Leu	Leu	Leu	Pro	Trp	Val	Ala	Gly	Gly	Val	Gly	Thr	Ser	Pro	Arg	Asp
		35				40						45			
Tyr	Trp	Leu	Pro	Ala	Leu	Ala	His	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly
	50				55					60					
Thr	Lys	Thr	Ala	Cys	Cys	Tyr	Gly	Trp	Lys	Arg	Asn	Ser	Lys	Gly	Val
65					70					75					80
Cys	Glu	Ala	Val	Cys	Glu	Pro	Arg	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly
				85					90					95	
Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser
			100					105					110		
Gln	Asp	Val	Asn	Glu	Cys	Ala	Phe	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg
		115					120					125			
Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His
	130				135						140				
Met	Leu	Leu	Pro	Asp	Ala	Thr	Cys	Ser	Asn	Ser	Arg	Thr	Cys	Ala	Arg
145					150					155					160

1011c2PCTSEQUENCE LISTING

Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys
 165 170 175
 Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys
 180 185 190
 Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn
 195 200 205
 Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile
 210 215 220
 Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile
 225 230 235 240
 Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys
 245 250 255
 Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg
 260 265 270
 Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His
 275 280

<210> 390

<211> 85

<212> PRT

<213> Rat

<400> 390

Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
 1 5 10 15
 Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
 20 25 30
 Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
 35 40 45
 Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
 50 55 60
 Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
 65 70 75 80
 Gln Thr Asn Ile Leu
 85

<210> 391

<211> 158

<212> PRT

<213> Rat

<400> 391

Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
 1 5 10 15
 Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
 20 25 30
 Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
 35 40 45
 Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
 50 55 60
 Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
 65 70 75 80
 Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
 85 90 95
 Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile

1011c2PCTSEQUENCE LISTING

			100						105					110			
Arg	Tyr	Asn	Ala	Thr	Met	Asp	Glu	Arg	Arg	Tyr	Met	Pro	Arg	Ala	His		
		115					120					125					
Leu	Asp	Glu	Gly	Ala	Asp	Gln	Phe	Thr	Asn	Arg	Ala	Val	Leu	Leu	Ser		
	130					135					140						
Ser	Gly	Gln	Glu	His	Cys	Gln	Arg	Ile	Asn	Phe	His	Val	Leu				
145					150					155							

<210> 392
 <211> 124
 <212> PRT
 <213> Mouse

<400> 392

Ala	Ala	Glu	Gln	Glu	Ala	Ser	Ser	Arg	Arg	Arg	Arg	Gly	Gly	Ala	Gly		
1				5				10						15			
Pro	Ala	Leu	Phe	Ser	Ser	Gly	Ser	Leu	Arg	Ser	Glu	Pro	Gln	Pro	Arg		
		20						25					30				
Leu	Pro	Gln	Ala	Arg	Ser	Arg	Pro	Arg	Pro	Ser	Phe	Leu	Gln	Ala	Arg		
		35					40					45					
Ser	Arg	Pro	Cys	Leu	Ser	Gln	Ala	Cys	Ser	Pro	Ala	Ala	Ser	Val	Leu		
	50					55					60						
Ser	Ser	Ser	Ser	Leu	Cys	Gly	Arg	Ser	His	Leu	Leu	Pro	Gly	Ser	Leu		
65				70						75					80		
Pro	Ala	Thr	Ala	Phe	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Leu	Pro	Gly	Arg		
			85						90					95			
Arg	Pro	Ser	Ala	Ala	Gln	Ala	Ala	Pro	Val	Leu	Ala	Trp	Gly	Leu	Val		
			100					105					110				
Ala	Phe	Gln	Leu	Gly	Val	Ala	Ala	Gly	Ala	Gly	Arg						
		115						120									

<210> 393
 <211> 242
 <212> PRT
 <213> Rat

<400> 393

Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Gly	Glu	Ala	Cys	Gly	Gln		
1				5				10						15			
Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ser	Ser	His	Leu	Val		
		20						25					30				
Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Thr	Gly	Pro	Glu	Glu		
		35					40					45					
Ser	His	Cys	Leu	Gln	Cys	Arg	Lys	Gly	Trp	Ala	Leu	His	His	Leu	Lys		
	50					55					60						
Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gln	Ala	Thr	Cys	Gly	Ala		
65				70						75					80		
Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg	Asp	Cys		
				85					90					95			
Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Pro	Cys	Lys		
			100					105					110				
Lys	Cys	Ser	Arg	Gly	Tyr	Gln	Gln	Val	Gly	Ser	Lys	Cys	Leu	Asp	Val		
		115				120						125					
Asp	Glu	Cys	Glu	Thr	Val	Val	Cys	Pro	Gly	Glu	Asn	Glu	Gln	Cys	Glu		
	130					135						140					

1011c2PCTSEQUENCE LISTING

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Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
145      150      155      160
Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
      165      170      175
Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
      180      185      190
Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
      195      200      205
Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
      210      215      220
Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
225      230      235      240
Gly Arg

```

<210> 394
 <211> 99
 <212> PRT
 <213> Mouse

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<400> 394
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Cys
 1      5      10      15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
      20      25      30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
      35      40      45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
      50      55      60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65      70      75      80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
      85      90      95
Tyr Glu Glu

```

<210> 395
 <211> 103
 <212> PRT
 <213> Human

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<400> 395
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1      5      10      15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
      20      25      30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
      35      40      45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
      50      55      60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65      70      75      80
Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
      85      90      95
Ser Gly Glu Arg Arg Pro Leu

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1011c2PCTSEQUENCE LISTING

100

<210> 396
 <211> 1529
 <212> PRT
 <213> Rat

<400> 396
 Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val
 1 5 10 15
 Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys
 20 25 30
 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
 35 40 45
 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
 50 55 60
 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
 65 70 75 80
 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
 85 90 95
 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
 100 105 110
 Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
 115 120 125
 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
 130 135 140
 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
 145 150 155 160
 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
 165 170 175
 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
 180 185 190
 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
 195 200 205
 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
 210 215 220
 Arg Gln Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
 225 230 235 240
 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
 245 250 255
 Cys Ser Gly His Gln Ser Phe Met Ala Pro Ser Cys Ser Val Leu His
 260 265 270
 Cys Pro Ile Ala Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly
 275 280 285
 Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu Thr Ile Thr Glu
 290 295 300
 Ile Arg Leu Glu Gln Asn Ser Ile Arg Val Ile Pro Pro Gly Ala Phe
 305 310 315 320
 Ser Pro Tyr Lys Lys Leu Arg Arg Leu Asp Leu Ser Asn Asn Gln Ile
 325 330 335
 Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg Ser Leu Asn Ser
 340 345 350
 Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro Lys Ser Leu Phe
 355 360 365
 Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys Ile

1011c2PCTSEQUENCE LISTING

370	375	380
Asn Cys Leu Arg Val	Asp Ala Phe Gln Asp Leu His Asn Leu Asn Leu	
385	390	395
Leu Ser Leu Tyr Asp	Asn Lys Leu Gln Thr Val Ala Lys Gly Thr Phe	400
	405	410
Ser Ala Leu Arg Ala Ile Gln Thr Met His Leu Ala Gln Asn Pro Phe		415
	420	425
Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr Leu His Thr Asn		430
	435	440
Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro Arg Arg Leu Ala		445
	450	455
Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe Arg Cys Ser Ala		460
465	470	475
Lys Glu Gln Tyr Phe Ile Pro Gly Thr Glu Asp Tyr Arg Ser Lys Leu		480
	485	490
Ser Gly Asp Cys Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys		495
	500	505
Glu Gly Thr Thr Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro		510
	515	520
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Ser Thr Leu Asn Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys His Leu		655
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 Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu
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 Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys
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 Arg Lys Glu Tyr Met Val Arg
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<210> 409
 <211> 590
 <212> PRT
 <213> Mouse

<400> 409
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 35 40 45
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Arg Glu Arg
 50 55 60
 Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
 65 70 75 80
 Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
 85 90 95
 Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
 100 105 110
 Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
 115 120 125
 Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
 130 135 140
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
 145 150 155 160
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
 165 170 175
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
 180 185 190
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
 195 200 205
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
 210 215 220
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
 225 230 235 240
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
 245 250 255
 Ala Ser Leu Ile Gly Ile Met Gln Arg Cys Trp His Ala Asp Pro Gln
 260 265 270
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
 275 280 285
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
 290 295 300

1011c2PCTSEQUENCE LISTING

Lys	Ser	Ser	Leu	Glu	Ser	Lys	Ser	Glu	Ala	Arg	Pro	Glu	Ser	Ser	Arg
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Leu	Lys	Arg	Ala	Ser	Ala	Pro	Pro	Phe	Asp	Asn	Asp	Cys	Ser	Leu	Ser
				325					330						335
Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Ile	Ser	Gln	Thr	Leu	Glu	Gly
			340					345					350		
Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Ser	Glu	Cys	Lys	Leu	Pro	Ser	Ser
		355				360						365			
Ser	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser	Ala	Phe
370					375						380				
Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Ala	Ser	Thr
385				390						395					400
Gly	Asp	Leu	Gly	Pro	Thr	Asp	Ile	Gln	Lys	Lys	Lys	Leu	Val	Asp	Ala
				405				410							415
Ile	Ile	Ser	Gly	Asp	Thr	Ser	Arg	Leu	Met	Lys	Ile	Leu	Gln	Pro	Gln
			420					425					430		
Asp	Val	Asp	Leu	Val	Leu	Asp	Ser	Ser	Ala	Ser	Leu	Leu	His	Leu	Ala
		435				440						445			
Val	Glu	Ala	Gly	Gln	Glu	Glu	Cys	Val	Lys	Trp	Leu	Leu	Leu	Asn	Asn
450					455						460				
Ala	Asn	Pro	Asn	Leu	Thr	Asn	Arg	Lys	Gly	Ser	Thr	Pro	Leu	His	Met
465				470						475					480
Ala	Val	Glu	Arg	Lys	Gly	Arg	Gly	Ile	Val	Glu	Leu	Leu	Leu	Ala	Arg
				485				490							495
Lys	Thr	Ser	Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala	Leu	His
			500					505					510		
Phe	Ala	Ala	Gln	Asn	Gly	Asp	Glu	Ala	Ser	Thr	Arg	Leu	Leu	Leu	Glu
		515				520						525			
Lys	Asn	Ala	Ser	Val	Asn	Glu	Val	Asp	Phe	Glu	Gly	Arg	Thr	Pro	Met
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His	Val	Ala	Cys	Gln	His	Gly	Gln	Glu	Asn	Ile	Val	Arg	Thr	Leu	Leu
545				550					555						560
Arg	Arg	Gly	Val	Asp	Val	Gly	Leu	Gln	Gly	Lys	Asp	Ala	Trp	Leu	Pro
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Leu	His	Tyr	Ala	Ala	Trp	Gln	Gly	His	Leu	Pro	Ile	Gly	Lys		
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 <212> DNA
 <213> Human

<400> 410

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 180
 ctggaagatc ataacagtta ctgcatcaac ggtgcttggt cattccacca tgagctagag
 240
 aaagccatct gcaggtgttt tactgggttat actggagaaa ggtgtctaaa attgaaatcg
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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Human

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 180
 aacggtgctt gtgcattcca ccatgagcta gagaaagcca tctgcagggtg tctaaaattg
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 <211> 460
 <212> DNA
 <213> Human

<400> 412
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 120
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 180
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 240
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 300
 ccaaaattaa agttttcaga tgaacaaca aaacttgctc agctgactag actcgaaaat
 360
 aatgaaagtt gggatcacaa tgaaatgaga agataaaatt cagcgttggc ctttagactt
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<210> 413
 <211> 112
 <212> PRT
 <213> Human

<400> 413
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 20 25 30
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 35 40 45
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
 50 55 60

1011c2PCTSEQUENCE LISTING

Asn	Ser	Tyr	Cys	Ile	Asn	Gly	Ala	Cys	Ala	Phe	His	His	Glu	Leu	Glu
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Lys	Ala	Ile	Cys	Arg	Cys	Phe	Thr	Gly	Tyr	Thr	Gly	Glu	Arg	Cys	Leu
				85					90					95	
Lys	Leu	Lys	Ser	Pro	Tyr	Asn	Val	Cys	Ser	Gly	Glu	Arg	Arg	Pro	Leu
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<210> 414
 <211> 94
 <212> PRT
 <213> Human

<400> 414

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			20					25					30		
Ala	Gln	Gln	Ala	Asp	Asn	Ile	Glu	Gly	Pro	Ile	Ala	Leu	Lys	Phe	Ser
		35					40					45			
His	Leu	Cys	Leu	Glu	Asp	His	Asn	Ser	Tyr	Cys	Ile	Asn	Gly	Ala	Cys
	50				55						60				
Ala	Phe	His	His	Glu	Leu	Glu	Lys	Ala	Ile	Cys	Arg	Cys	Leu	Lys	Leu
65					70					75					80
Lys	Ser	Pro	Tyr	Asn	Val	Cys	Ser	Gly	Glu	Arg	Arg	Pro	Leu		
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<210> 415
 <211> 73
 <212> PRT
 <213> Human

<400> 415

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			20					25					30		
Asp	His	Asn	Ser	Tyr	Cys	Ile	Asn	Gly	Ala	Cys	Ala	Phe	His	His	Glu
		35					40					45			
Leu	Glu	Lys	Ala	Ile	Cys	Arg	Cys	Leu	Lys	Leu	Lys	Ser	Pro	Tyr	Asn
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<210> 416
 <211> 312
 <212> DNA
 <213> Human

<400> 416

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 180

1011c2PCTSEQUENCE LISTING

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 312

<210> 417
 <211> 103
 <212> PRT
 <213> Human

<400> 417
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 35 40 45
 His Leu Cys Leu Gly Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys
 50 55 60
 Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Phe Thr Gly
 65 70 75 80
 Tyr Thr Gly Glu Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
 85 90 95
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<210> 418
 <211> 846
 <212> DNA
 <213> Rat

<400> 418
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 540
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1011c2PCTSEQUENCE LISTING

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 840
 gaacct
 846

<210> 419
 <211> 960
 <212> DNA
 <213> Mouse

<400> 419
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 420
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 840
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<210> 420
 <211> 1330
 <212> DNA
 <213> Mouse

<400> 420

1011c2PCTSEQUENCE LISTING

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<210> 421
<211> 880
<212> DNA
<213> Mouse

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<400> 421
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1011c2PCTSEQUENCE LISTING

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480
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<210> 422
 <211> 533
 <212> DNA
 <213> Mouse

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<400> 422
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420
aaggcactgt ttgaagcaca ggccatgaag taagacttgc tttctagtta aattgagggt
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<210> 423

1011c2PCTSEQUENCE LISTING

<211> 738

<212> DNA

<213> Rat

<400> 423

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 720
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 738

<210> 424

<211> 1035

<212> DNA

<213> Rat

<400> 424

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 180
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 360
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 aggggtgcca ccagagctgc agattgcgtt catggcttct ctagcgactc acttcagcaa
 480
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1011c2PCTSEQUENCE LISTING

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 720
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 780
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<210> 425

<211> 835

<212> DNA

<213> Rat

<400> 425

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 480
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 720
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1011c2PCTSEQUENCE LISTING

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 <211> 1337
 <212> DNA
 <213> Mouse

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 <222> (626)...(626)

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 780
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 1080
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 1200
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1011c2PCTSEQUENCE LISTING

1337

<210> 427
 <211> 780
 <212> DNA
 <213> Mouse

<400> 427

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 660
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 780

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<210> 428
 <211> 460
 <212> DNA
 <213> Mouse

<400> 428

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 120
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catagttcat atcgagggg agttcaaaga catggatgcc acttcagaat taaagaataa
 240
gacatttgat accttaagga atcaccatc tttttatgtg ttttaaccatc gtggctcagt
 300
gctgttccgg ccttcagatg caacaaattc ttcaaaccta gatgcattgt cctctaatac
 360
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 420

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1011c2PCTSEQUENCE LISTING

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460

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<211> 472
<212> DNA
<213> Mouse

<400> 429
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472

<210> 430
<211> 954
<212> DNA
<213> Mouse

<400> 430
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300
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420
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1011c2PCTSEQUENCE LISTING

720
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 840
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<210> 431
 <211> 780
 <212> DNA
 <213> Mouse

<400> 431
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 660
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 780

<210> 432
 <211> 1144
 <212> DNA
 <213> Mouse

<400> 432
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 120
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 180

1011c2PCTSEQUENCE LISTING

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 1144

<210> 433
 <211> 438
 <212> DNA
 <213> Mouse

<400> 433
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1011c2PCTSEQUENCE LISTING

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438

<210> 434
<211> 383
<212> DNA
<213> Mouse

<400> 434
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<210> 435
<211> 405
<212> DNA
<213> Rat

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<221> unsure
<222> (353)...(353)

<221> unsure
<222> (387)...(388)

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360

1011c2PCTSEQUENCE LISTING

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405

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<211> 151
<212> DNA
<213> Rat

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151

<210> 437
<211> 1715
<212> DNA
<213> Mouse

<400> 437
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960
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1011c2PCTSEQUENCE LISTING

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 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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 1627

<210> 439
 <211> 2401
 <212> DNA
 <213> Mouse

<400> 439
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1011c2PCTSEQUENCE LISTING

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<211> 2250

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<213> Mouse

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<221> unsure

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<211> 1685

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<221> unsure

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1011c2PCTSEQUENCE LISTING

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<212> DNA

<213> Rat

<400> 447

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Rat

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1011c2PCTSEQUENCE LISTING

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<211> 936

<212> DNA

<213> Rat

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<212> DNA

<213> Mouse

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<211> 1225

<212> DNA

<213> Mouse

<400> 451

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1011c2PCTSEQUENCE LISTING

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 <212> DNA
 <213> Mouse

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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<211> 1121

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<213> Rat

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1011c2PCTSEQUENCE LISTING

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 420
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 1121

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 35 40 45
 Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His Met Leu Pro
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<210> 457
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1011c2PCTSEQUENCE LISTING

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 Met

<210> 458
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 35 40 45
 Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys Pro Gln Asp
 50 55 60
 Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg Asn Gly Gly
 65 70 75 80
 Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met
 85 90 95
 Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala
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 Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr
 115 120 125
 Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu
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 Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln Arg Val Cys
 145 150 155 160
 Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Arg Cys Leu
 165 170 175
 Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly Cys Lys Pro
 180 185 190
 Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys Pro Thr Gly
 195 200 205
 Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg
 210 215 220
 Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro
 225 230 235 240
 Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Ala Asp Cys Asp Pro
 245 250 255
 Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly Pro Thr Cys
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1011c2PCTSEQUENCE LISTING

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 35 40 45
 Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Ser
 50 55 60
 Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile Cys Ile Asn
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 <211> 53
 <212> PRT
 <213> Mouse

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<210> 461
 <211> 261
 <212> PRT
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 35 40 45
 His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu Leu Thr His
 50 55 60
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 Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg Lys Phe Val
 85 90 95

1011c2PCTSEQUENCE LISTING

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 165 170 175
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 Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Asn
 195 200 205
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<400> 462
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 Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln Tyr Glu Asp
 35 40 45
 Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln Val Thr Thr
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 Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile Phe Thr Leu
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 Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg Val Arg Leu
 85 90 95
 Val Phe Gln Asp Ser Pro Val His Gly Arg Lys Leu Arg Ser Glu
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<210> 463
 <211> 314
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1011c2PCTSEQUENCE LISTING

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	35	40	45
Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr			
	50	55	60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly			
	65	70	75
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His			
	85	90	95
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys			
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Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln			
	115	120	125
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Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu			
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Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly			
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	195	200	205
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly			
	210	215	220
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	225	230	235
Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala			
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<210> 464

<211> 1663

<212> DNA

<213> Mouse

<400> 464

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1011c2PCTSEQUENCE LISTING

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 1663

<210> 465

<211> 99

<212> PRT

<213> Mouse

<400> 465

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1011c2PCTSEQUENCE LISTING

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Lys	Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
		35					40					45				
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Val	Thr	Thr	Lys	Ser	Met	Ser	
	50					55					60					
Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	Ser	Thr	
65					70					75					80	
Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	Arg	Arg	Val	
				85					90					95		
Tyr	Glu	Glu														

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
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PCT

(10) International Publication Number
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14/485, 14/515, 7/06, C12N 15/63, 15/85, A61K 38/08,
38/17, A61P 17/00, 25/00, 29/00, 35/00, 43/00

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(21) International Application Number: **PCT/NZ00/00075**

(74) Agents: **BENNETT, Michael, Roy et al.**; West-Walker Bennett, Mobil on the Park, 157 Lambton Quay, Wellington (NZ).

(22) International Filing Date: **15 May 2000 (15.05.2000)**

(25) Filing Language: **English**

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(30) Priority Data:
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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

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Published:

— *With international search report.*

(88) Date of publication of the international search report:
15 February 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE**

(57) Abstract: Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

WO 00/69884 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00075

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. ⁷: C07K 14/47, 14/485, 14/515, 7/06; C12N 15/63, 15/85, A61K 38/08, 38/17; A61P 17/00, 25/00, 29/00, 35/00, 43/00.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

ANGIS: Sequence search; ID No. 187, 196, 342, 343, 395, 397, 398.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochemical and Biophysical Chemical Research Communications. 225:703-706 (1999) Hromas, R et al "Cloning of BRAK, a Novel Divergent CXC Chemokine Preferentially Expressed in Normal versus Malignant Cells" See Figure 1, Table 1. Sequence ID No. 397 and No. 398, both 100%.	1-8, 13-14, 15-16, 17, 23, 25
P,X	<i>J Immunol</i> 2000 Sep 1;165(5):2588-95 Cao X, Zhang W, Wan T, He L, Chen T, Yuan Z, Ma S, Yu Y, Chen G "Molecular cloning and characterization of a novel CXC chemokine macrophage inflammatory protein-2 gamma chemoattractant for human neutrophils and dendritic cells." See whole document. Sequence ID No. 397 and No. 398, both 100% homology.	1-28



Further documents are listed in the continuation of Box C



See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

12 October 2000

Date of mailing of the international search report

7 NOV 2000

Name and mailing address of the ISA/AU

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Facsimile No. (02) 6285 3929

Authorized officer

I. D. Dowd.

IAN DOWD

Telephone No : (02) 6283 2273

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00075

Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See supplemental sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to:
The invention as it is exemplified by amino acid sequence ID No.s 187, 196, 342, 343, 395, 397, and 398.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

This international application does not comply with the requirement of unity of invention because it does not relate to one invention or to a group of invention so linked as to form a single general inventive concept:

(1) The international application has claimed nucleic acid sequences encoding 4 enzymes and 31 proteins, the fragments, complements, reverse complements and reverse sequences of these genes, expression vectors of the sequences, transformed host cells, methods for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularization of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of HIV-1 to leukocytes, treatment of inflammatory and neurological diseases and cancer, and polypeptides coded by these genes and their variants with at least 50%, 75% or 90% identity.

(2) Whilst the 465 sequences are from skin cells, the claims are defined as to these sequences per se and their variants which have 50%, 75% or 90% identity. The invention as claimed is also to the various methods of use (as indicated above) based on these sequences. It is clear that all these nucleic acid sequences are not limited to the source from which they are isolated, as such the source from skin cells can not be the special technical feature under Rule 13.2 of the PCT.

(3) The nucleic acid sequences and their putative amino acid sequences have been shown to have similarity to proteins or enzymes which are known (see Table 2 pages 24 to 25 of the description). Based on this methodology, the 465 sequences have been assigned to 31 proteins and 4 enzymes. However, these proteins and enzymes are not unified by sequence homology, by a common substrate or their mode of action. Additionally, many of these proteins or enzymes are known to have activity not directly associated with epithelial cells. Therefore, the use of nucleotide sequences encoding these proteins and enzymes, either in the sense or anti-sense direction, is not a special technical feature under Rule 13.2 of the PCT.

For the above reasons, this international application does not comply with the requirements of unity of invention.

The International Searching authority has found that there are 34 separate inventions, wherein a single protein or enzyme provides the special technical feature.

1. Polynucleotide Sequence ID No. 118 and amino acid Sequence ID No. 196 and their at least 50% identity homologues, encoding human TR1.
2. Polynucleotide Sequence ID No. 68, 437 and amino acid Sequence ID No. 187 and their at least 50% identity homologues, encoding transforming growth factor alpha, murine TR1.
3. Polynucleotide Sequence ID No. 119 and amino acid Sequence ID No. 197 and their at least 50% identity homologues, encoding DP3.
4. Polynucleotide Sequence ID No. 271 and amino acid Sequence ID No. 345 and their at least 50% identity homologues, encoding MURINE KS1.
5. Polynucleotide Sequence ID No. 272 and amino acid Sequence ID No. 346 and their at least 50% identity homologues, encoding human KS1.

Continued on supplemental sheet

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

6. Polynucleotide Sequence ID No. 273 and amino acid Sequence ID No. 347 and their at least 50% identity homologues, encoding KS2.
7. Amino acid Sequence ID No. 129 and their at least 50% identity homologues, encoding KS3.
8. Polynucleotide Sequence ID No. 64 and 372 and amino acid Sequence ID No. 183 and 396 and their at least 50% identity homologues, encoding Slit (a secreted molecule required for CNS development).
9. Polynucleotide Sequence ID No. 65 and amino acid Sequence ID No. 184 and their at least 50% identity homologues, encoding an immunoglobulin receptor.
10. Polynucleotide Sequence ID No. 66, 403 and amino acid Sequence ID No. 185, 409 and their at least 50% identity homologues, encoding RIP protein kinase.
11. Polynucleotide Sequence ID No. 67 and amino acid Sequence ID No. 186 and their at least 50% identity homologues, encoding extracellular protein.
12. Polynucleotide Sequence ID No. 69 and amino acid Sequence ID No. 188 and their at least 50% identity homologues, encoding DRS protein.
13. Polynucleotide Sequence ID No. 70 and amino acid Sequence ID No. 189 and their at least 50% identity homologues, encoding A33 receptor.
14. Polynucleotide Sequence ID No. 71 and amino acid Sequence ID No. 190 and their at least 50% identity homologues, encoding IL-12 alpha sub-unit.9. Polynucleotide Sequence ID No. 72 and amino acid Sequence ID No. 191 and their at least 50% identity homologues, encoding TNF receptor.
15. Polynucleotide Sequence ID No. 73, 438 and amino acid Sequence ID No. 192, 458 and their at least 50% identity homologues, encoding epidermal growth factor.
16. Polynucleotide Sequence ID No. 74 and amino acid Sequence ID No. 193 and their at least 50% identity homologues, encoding fibronectin type III receptor.
17. Polynucleotide Sequence ID No. 75, 439 and amino acid Sequence ID No. 194, 459 and their at least 50% identity homologues, encoding serine/threonine kinase.
18. Polynucleotide Sequence ID No. 76 and amino acid Sequence ID No. 195 and their at least 50% identity homologues, encoding immunoglobulin receptor.
19. Polynucleotide Sequence ID No. 254 and amino acid Sequence ID No. 331 and their at least 50% identity homologues, encoding immunoglobulin-like receptor.
20. Polynucleotide Sequence ID No. 255 and amino acid Sequence ID No. 332 and their at least 50% identity homologues, encoding epidermal growth factor.
21. Polynucleotide Sequence ID No. 256 and amino acid Sequence ID No. 333 and their at least 50% identity homologues, encoding serine/threonine kinases.

Continued on supplemental sheet

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No:

22. Polynucleotide Sequence ID No. 257 and amino acid Sequence ID No. 334 and their at least 50% identity homologues, encoding protein kinase.
23. Polynucleotide Sequence ID No. 258 and amino acid Sequence ID No. 335 and their at least 50% identity homologues, encoding notch family proteins.
24. Polynucleotide Sequence ID No. 259 and amino acid Sequence ID No. 336 and their at least 50% identity homologues, encoding extracellular protein with epidermal growth factor domain.
25. Polynucleotide Sequence ID No. 260, 453 and amino acid Sequence ID No. 337, 463 and their at least 50% identity homologues, encoding fibronectin Type III receptor.
26. Polynucleotide Sequence ID No. 261 and amino acid Sequence ID No. 338 and their at least 50% identity homologues, encoding immunoglobulin receptor.
27. Polynucleotide Sequence ID No. 262, 454 and amino acid Sequence ID No. 339 and their at least 50% identity homologues, encoding ADP/ATP transporter.
28. Polynucleotide Sequence ID No. 263 and amino acid Sequence ID No. 340 and their at least 50% identity homologues, encoding mouse CXC chemokine.
29. Polynucleotide Sequence ID No. 264 and amino acid Sequence ID No. 341 and their at least 50% identity homologues, encoding nucleotide sugar transporter.
30. Polynucleotide Sequence ID No. 365 and amino acid Sequence ID No. 389 and their at least 50% identity homologues, encoding TGF-betas.
31. Polynucleotide Sequence ID No. 366 and amino acid Sequence ID No. 390 and their at least 50% identity homologues, encoding integrins (membrane protein).
32. Polynucleotide Sequence ID No. 367 and amino acid Sequence ID No. 391 and their at least 50% identity homologues, encoding integrins.
33. Polynucleotide Sequence ID No. 368 and amino acid Sequence ID No. 392 and their at least 50% identity homologues, encoding cell wall protein precursor.
34. Polynucleotide Sequence ID No. 369 and amino acid Sequence ID No. 393 and their at least 50% identity homologues, encoding HT protein.